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1: geneseqp1990s:*
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1065.101 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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This invention describes the isolation of a novel human secreted protein, zsig46 encoded by a gene on chromosome 13 which is mainly expressed in the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zsig46, which may be associated with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschsprung's disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger syndrome). Antibodies and other binding proteins, are used as immunoassay

New secreted polypeptide, zsig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or diseases involving genes on chromosome 13.

Claim 3; Page 90-91; 101pp; English.

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω U	32	<u>ω</u>	30	29	28	27	26
83.5	84.5	85.5	85.5	98	98	86.5	87	87	87	87.5	88	88	88.5	88.5	88.5	89	89.5	89.5	91
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Aab52581	Aar37508	Aar25450	Aau74922	Abu32653	Abb49050	Abb92540	Aaw15565	Aaw58861	Aab34827	Aae06730	Abu31122	Abu32174	Aam41004	Aam39218	Add14088	Abb60986	Abg70004	Aaw41856	Aau33184
Helicobac	Human DNA	MH mutant	Synthetic	Protein e	Listeria	Herbicida		T. haloph	Gene 17 h	Human CAS	Protein e	Protein e	Human pol	Human pol	Human src	Drosophil	Larval vi	Ragweed p	Novel hum

ALIGNMENTS

RESULT 1 AAW92967

AAW92967 standard; protein; 346 AA.

14-MAY-1999

(first entry)

AAW92967;

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Secreted protein; zsig46; human; chromosome 13; thyroid; disease; hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cancer; Hirschspring's disease; neuronal ceroid-lipofucinosis; Wilson disease; Reiger syndrome; immunoassay; detection; anti-idiotypic antibody;
                                                                                                                     N-PSDB;
                                                                                                                                           Sheppard PO,
                                                                                                                                                                          24-JUL-1997;
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                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                   therapy; diagnostic.
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                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obseity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
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RESULT 3
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19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZ24811-Z24907; amino acid sequences AAX41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the
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Wei Y,
Shi Y,
                                                                                                                                                                                                                                                                                                                                                                                                       new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 95 polynucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes, useful cancers, neurological disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders.
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                                                                                                                                                                                                                                                                                                                                                                               Sequence
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DB; AAZ24826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a secreted human protein encoded by the
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, Endress GA,
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                                                  ETNYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIF
                                                                                                                       NQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNI
                                                                                                                                                                            MEWYELFOLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMF
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                      DAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                                       NOMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNI
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                                                                                                                                                                                                                                KYTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYT
DAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                                                                                              MEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMF
                                                                                                                                                                                                                                                                      MRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDPYCQA
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98US-0078579P.
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Pred. No. 1.1e-184;
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une diseases,
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R, Lafleur DW,
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clones. 830 cDNA molecules encoding a human protein have been isolated and muleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful. for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; SEQ ID NO 3978; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 Primers useful for synthesizing full length cDNA clones and in genetic manipulation.
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                                         DAVIVHKQEYLEYNEEYWELPMKEPFIKITYEEIPLPIRNKTLSGL 346
                                                                                                                   ETNYTRIFLYSGEPTYLGNETSVEGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIF 300
                                                                                                                                                                                   NQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNI 252
                                                                                                                                                                                                              NQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNI 240
                                                                                                                                                                                                                                                                              MEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMF
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                                                                                        ETNYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIF
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2000JP-00118774.
2000JP-00183765.
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Sugiyama T, Nagai K, Kojima
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Pred. No. 2.2e-184;
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Best Local
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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100.0%; Prr
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Pred. No. 4.8e-81;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234637P.
27-SEP-2000; 2000US-0234637P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
17-OCT-2001
                                                     AAM32740;
                                                                                                    AAM32740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #6745
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                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                    standard;
                                                                                                                                                                                                                                                                            IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 346
                                                                                                                                                                                                                                             IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                                                                                                                                                                                                                                                                                  YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV 120
                                                                                                                                                                                                                                                                                                                                                                                                  YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
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(first
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                                                                                                    protein;
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100.0%;
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Pred. No. 4.8e-8:
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                       Human; gene expression; heart; microarray; vascular system, cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
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                                                               Protein #6079
                                                                                          23-JAN-2002
                                                                                                                   ABB24080;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide #6777 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n genome-derived single exon nucleic expression in human placenta.
                                                                                                                                                                                                                                   304
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                                                                                                                                           standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 33009; 654pp;
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                                                                                                                                                                                                                                                                                                                                                                46.0%;
ilarity 100.0%;
Conservative
                                                                                         (first entry)
                                                               encoded by probe
                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                             163
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; Pred. No. 4.8e-81;
0; Mismatches 0;
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                                                               for measuring heart cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                         Length 163
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                                                                                                                                                                                                            163
                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                 expression
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congenital heart disease.

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Best Local Similarity
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                                        Human; bone marrow expressed exon; gene expression analysis; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
Homo sapiens
                                                                                                             Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                           06-NOV-2001
                                                                                                                                                                                                        AAM72492;
                                                                                                                                                                                                                                                 AAM72492 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 163
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27-SEP-2000;
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26-MAY-2000;
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2000US-0207456P.
2000US-00608409.
2000US-00632366.
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2000US-0236359P.
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                                                                                                                                                                                                                                                   163
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                                                                  probe;
                                                                                                             32798.
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RESULT 9
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Best Local Similarity
Matches 163; Conserv
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                              05-NOV-2001
                                                                                                                                                                                                         AAM59901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
            30-JAN-2001; 2001WO-US000667.
                                      09-AUG-2001
                                                           WO200157275-A2
                                                                                       Homo sapiens
                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 32006.
                                                                                                                                                                                                                                  AAM59901 standard; protein; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; SEQ ID NO 32798; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-488900/53.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                 IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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2000US-0207456P.
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                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.0%; Score 886; DB 4; 1
100.0%; Pred. No. 4.8e-81;
^ Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
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Best Local S
Matches 163
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26-MAY-2000;
30-JUN-2000;
31-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 32006; 650pp + Sequence Listing;
                                                                                30-JAN-2001; 2001WO-US000664
                                                                                                         09-AUG-2001
                                                                                                                                                                             hypercholesterolaemia; coronary
                                                                                                                                                                                                                                        25-FEB-2003
                                                                                                                                                                                                                                                                                      ABG54183 standard; peptide; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 163 AA;
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                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163;
                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                             liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; holesterolaemia; coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
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2000US-0207456P.
2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
           ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention provides a number of single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probes
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                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                        entry)
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100.0%;
                                                                                                                                                                                                                 SEQ ID No 32831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 886;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 4;
. 4.8e-81;
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WO200186003-A2

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RESULT 11
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                                                                                                                            Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; thermansky-pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                       Human peptide
                                                                                                                                                                                                                                                                                                                        19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                          ABG42312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                   hyaline membrane
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                                                                                 sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome-derived single exon nucleic acid probes useful expression in human adult liver.
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                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVHKQFYLFYNFEYWFLPMKFDFIKITYEEIPLPIRNKTLSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVHKOFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
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                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                       encoded by genome-derived single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO 32831;
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                                                                                                                     disease.
                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Er
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                          163
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Pred. No. 4.8e-81;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 163;
                                                                                                                                                                                                                                                                                        SEQ ID 31977.
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array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung tisease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, buildenous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-pudlak syndrome. Sarcidosis nulmonary hasmasiderosis evidences.
                                                                                      Matches
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                          dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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26-MAY-2000;
30-JUN-2000;
30-AUG-2000;
21-SEP-2000;
27-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes. Also included are a microarray comprising the novel set of probes the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample
                                                                                                                                                                                                                                       Sequence 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spatially-addressable set of single exon nucleic acid probes, used
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184 AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                      163;
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from human lung, comprising (a) contacting the array with a ion of detectably labeled nucleic acids derived from human lung (b) measuring the label detectably bound to each probe of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-0236359P.
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100.0%;
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Pred. No.
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of.

244 YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV

303 60

AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN

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                         metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ov cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder;
       further be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to 2175 novel human ovarian antigens ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABQ55979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; chromosome mapping;
antibody preparation; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP42902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4034; 2922pp; English
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   gene
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   therapy,
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   chromosome mapping,
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immunomodulatory; neuroprotective;
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       in the
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Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-2000;
30-MAR-2001;
01-MAY-2001;
05-JUN-2001;
25-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                Jackson
Siemers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antipsoriatic; cardiant; cytostatic; gene therapy; liver disease; proliferative disorder; renal failure; cardiovascular disorder; immunological disorder; arthritis; psoriasis; congenital heart defect;
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                    The invention relates to a novel isolated nucleic acid comprising a polynucleotide having a nucleotide sequence selected from 40 polynucleotides fully defined in the specification. The polynucleotide the invention has antiproliferative, hepatocropic, nephrotropic, antiproriatic, cardiant, and cytostatic activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2001; 2001WO-US050459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-2003
  polynucleotide
                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                          WPI; 2002-599721/64.
                                                                                                                                                                                                                                                                                                                                                                        Krystek
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                                                                                                                                                                                                                                              el polynucleotides encod:
prevention or treatment
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; 2001US-0280186P.
; 2001US-0287735P.
; 2001US-0295848P.
; 2001US-0300465P.
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  may have a use
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     a use in gene therapy. A polymucleotide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; human; mouse; yeast;
                                                                                                                                                                        English
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                                                                                                                                                                                                                                                                                                                                                                                                Mintier G, Ramanat
Finger J, Todderud
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No. 1.4e-39;
                                                                                                                                                                                                                                                                                                                                                                              Banas
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odderud CG, Bassolino
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Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide of the invention is useful for preventing, treating or ameliorating a medical condition, e.g. a proliferative disorder. They are also useful for treating e.g. liver disease, renal failure, immunological disorders including arthritis and psoriasis, cardiovascular disorders such as congenital heart defects and congestive heart failure, and cancer. A method of the invention is useful for diagnosing a pathological condition or susceptibility to a condition in a subject. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1705 AA;
                                                                        23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 7014
                                                                                                                                                                                                                                                                                                   ABB60074;
                                                                                                                                                                                                                                                                                                                           ABB60074 standard;
  WPI; 2001-656860/75
                          Venter JC,
                                                                                                             23-MAR-2001; 2001WO-US009231.
                                                                                                                                      27-SEP-2001
                                                                                                                                                             WO200171042-A2
                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                             pharmaceutical.
                                                                                                                                                                                                                          Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKFVLRTENKLAEFGAEFKNIETNYTRIFLYSG---EPTYLGNE--TSVFG---PTGNKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFW-CNQGAACFFEGIDDVHWKENGTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLEASWSDASGDQDSYQLLLYHPESHTLACNVSVSPDTLSYNFGDLLPGSQYVLEVITWA
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                                                 CORP NY.
                                                                                                                                                                                                                          developmental
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                           Adams M,
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2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -PGTPYQLKICAAAGPHQIWGPNAT--
                           Myers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
                                                02-JAN-2001; 2001US-0259302P
                                                                                                    28-DEC-2001;
                                                                                                                                                             29-AUG-2002
                                                                                                                                                                                                                 WO200266501-A2
                                                                                                                                                                                                                                                                       Helicobacter pylori
                                                                                                                                                                                                                                                                                                                        Protein-protein interaction; ulcer; selected interacting domain; SID
                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori selected interacting domain (SID) protein #1651.
                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU52308 standard; protein; 429 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2703 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABL04177
(HYBR-) HYBRIGENICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSLAPKEETIIEV----ELTNIQKKYY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLQNNISELFSLINFLEPSQFSSQEEFMSEFGSLRTEEEVNKLQALLKPMMLRRLKDDVE
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                                                                                                       2001WO-EP015428
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                                                                                                                                                                                                                                                                                                                                                                                                                            used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed at the top of the pages in the specification has obscured areas of protein sequence, the indexer has replaced the residue with an X to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 618; 642pp; English.
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                                                                                                                            201 LNFVGATEINIA--GATFKNLKTTSQNSYMTFMALGD--
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                                                                                                                                                                                                                                                                                                                    l Similarity
62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in mammals.
                                                                                                                                            SKFVLRTENKLABFGAEFKNIET---NYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAI 276
                                                                                                                                                                                                                                                                                      FRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCN-----QGAACFFEGIDDVHWK 164
FKFQGKTTIEKSVLSDASYTFDG
                             FPFI-KITYEEIPLPIRNKTLSG
                                                              SDFYDWTGGGYDFTGN--
                                                                                            KRFY----YPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLF-----
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Pred. No. 2.3;
28; Mismatches
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/pcodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/pcodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/pcodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/pcodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/pcodata/2/iaa/PCTUS_COMB.pep:*
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   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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US-09-157-021-31
US-09-156-842-31
US-09-1514-31
US-09-1514-31
US-09-159-1514-31
US-09-134-000C-3624
US-09-134-000C-3624
US-09-134-078-24
US-09-079-030-217
US-08-989-299-10
US-09-104-4228-27
US-09-104-4228-27
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US-09-105-252-991A-26565
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US-09-489-039A-11849
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US-09-134-000C-6185
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31, Appl
31503, Appl
24, Appl
24, Appl
27, Appl
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RESULT 1 US-09-108-006C-1 Sequence 1, Application US/09108006C Patent No. 6524613 GENERAL INFORMATION: APPLICANT: Steer, Clifford J. Kran, Betsy T. Bandyopadhyay, Paramita Roy-Chowdhury, Jayanta TITLE OF INVENTION: Hepatocellular Chimeraplasty NUMBER OF SEQUENCES: 62 CORRESPONDENCE ADDRESS: ADDRESSEE: Kimeragen, Inc. STREET: 300 Pheasant Run CIT: NewCom STATE: PA COUNTURE: 18940 COMPUTER REBABLE FORM: MEDIUM TYPE: Diskette COMPUTER: REBABLE FORM: MEDIUM TYPE: Diskette COMPUTER: APPLICATION NUMBER: US/09/108,006C FILING DATE: 30-Um-1992 CORRENT APPLICATION NUMBER: 60/54,288 FILING DATE: 30-APR-1997 APPLICATION NUMBER: 60/54,837 FILING DATE: 10-AVC-1997 APPLICATION NUMBER: 60/64,996 FILING DATE: 10-AVC-1997 APPLICATION NUMBER: 60/64,996 FILING DATE: 10-AVC-1997 APPLICATION NUMBER: 60/054,837 FILING DATE: 10-AVC-1997 APPLICATION NUMBER: 60/054,996 FILING DATE: 10-AVC-1997 APPLICATION NUMBER: 60/054,996 FILING DATE: 10-AVC-1999 APPLICATION NUMBER: 60/054,996 FILING DATE: 10-AVC-1999 APPLICATION NUMBER: 20258 REGISTRATION NUMBER: 20258 REGISTRATION NUMBER: 20258 REGISTRATION NUMBER: 20258 REFERENCE/DOCKET NUMBER: 7991-015-999 TELEPONNE: 215-504-4444 TELEPAX: 215-504-4444 TELEPAX: 215-504-4444 TELEPAX: 215-504-4444 TELEPAR: 215-504-4444 TELEPAR: 215-504-4444 TELEPAR: 215-504-4545 LEGUICH: 453 amino acids TYPE: amino acids	ALIGNMENTS	28 77.5 4.0 626 3 US-09-351-215-2 29 77 4.0 198 4 US-09-252-991A-19295 30 77 4.0 238 3 US-08-634-475-6 31 77 4.0 238 3 US-08-634-475-6 31 77 4.0 238 4 US-09-709-791-6 32 77 4.0 501 2 US-08-781-802-4 34 77 4.0 501 2 US-08-781-802-6 35 77 4.0 501 3 US-08-694-078-6 36 77 4.0 501 3 US-08-694-078-6 37 74.0 501 3 US-08-694-078-6 38 77 4.0 501 3 US-09-058-260-4 40, 77 4.0 501 3 US-09-058-260-2 41, 77 4.0 501 3 US-09-058-260-2 42 77 4.0 501 3 US-09-058-260-2 43 77 4.0 501 3 US-09-058-260-2 44 77 4.0 501 3 US-09-058-260-2 45 77 4.0 501 3 US-09-058-260-2 47 77 4.0 501 3 US-09-058-260-2 48 77 4.0 501 3 US-09-058-260-2 49 77 4.0 501 3 US-09-058-260-2 40 77 4.0 501 3 US-09-058-260-2 41 77 4.0 501 3 US-09-058-260-2 42 77 4.0 501 3 US-09-058-260-2 43 77 4.0 501 3 US-09-058-260-3 44 77 4.0 615 4 US-09-107-532A-6507
		Sequence 2, Appli Sequence 19295, A Sequence 6, Appli Sequence 6, Appli Sequence 5259, Ap Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 14, Appli Sequence 20, Appli Sequence 22, Appli Sequence 24, Appli Sequence 24, Appli Sequence 27, Appli Sequence 28, Appli Sequence 21, Appli Sequence 22, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli

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                                        JS-07-792-600-31
                                                                                                                          FILING DATE: 19911115
CLASSIFICATION: 435
ATTORNBY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: STDU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-838
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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Best Local S
Matches 58
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/792,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: COPELAND, WILLIAM C.
APPLICANT: WANG, TEREA S.-F.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC SYNTHESIS OF NUCLEIC ACID
                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Peter G. Carroll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                           TOPOLOGY:
                                                                                            TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 220 Montgomery Street, CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                    LENGTH:
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Pred. No.
Score 88.5;
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LENGTH: 1462
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                                                                                                                                                                                                                                                                                                                                                         Matches
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Patent No. 610002
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Copeland, William C. APPLICANT: Wang, Teresa S. F. TITLE OF INVENTION: Drug Design Assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: STDU-03484
CURRENT APPLICATION NUMBER: US/09/157,021A
CURRENT FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1991-11-15 NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 07/792,600
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                     4.6%; Score 88.5; Local Similarity 20.3%; Pred. No. 2. nes 71; Conservative 56; Mismatch.
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384
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                                                                                                     VKASP---EKGAET----WFDSYD---CSKFVLRTFNKLAEFGAE----
                                                                                                                                       WDKES-----EPAEEVKQEADSGKGTV----SYLGSFLPDVSCWDIDQEGDSSFSVQEVQ 323
                                                                                                                                                                                                                                              QAPVWEFKYGDLLGHLKIMHDAIGFRSTLIGKNYTMEWYELFOLGNCTFPHLRPEMDAPF 145
                                                                                                                                                                                                                                                                                                                      KREDERPKPDPYCQAKYTECPTG-----
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                               ETNYTRIFLYSGEPTYLGNETSVFGPTGNKT-LGLAIKRFYYPFKPHLPTKEFLLSLLQI
                                                                     VDSSHLPIVKGADEEQVFHFYWLDAYEDQYNQPGVVFLFGKVWIESAETHVSCCVMVKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYE----EIPLPIRNKTLS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERT-----LY-----FLPREMKIDLNTGKETGTPISMKDVYEEFDEKIATKYKIMK----
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-LY----FLPREMKIDLNTGKETGTPISMKDVYEEFDEKIATKYKIMK----
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6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         Mismatches
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APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Screening
FILE REFERENCE: STDU-03485
CURRENT APPLICATION NUMBER: US/09/156,842A
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 07/792,600
EARLIER FILING DATE: 1991-11-15
                                                                                                                                                                                                                                                                           Sequence 31, Application US/09591514 Patent No. 6670161
                                                                                                                                                                                                                                                        Patent No. 6670161
GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 31
                                   CURRENT APPLICATION NUMBER: US/09/591,514
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US/09/157,021
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 07/792,600
PRIOR FILING DATE: 1991-11-15
PRIOR FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                            APPLICANT: Copeland, William C. APPLICANT: Wang, Teresa S. F. TITLE OF INVENTION: Drug Design Assay FILE REFERENCE: STDU-03484
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ORGANISM: Homo sapiens
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o. 6103473
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Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342 SEQ ID NO 13503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6610836 GENERAL INFORMATION:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PHENONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 608
TYPE: PRT
ORGANISM: Klebsiella
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ORGANISM: Homo
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67; Conserv
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  DAEDAAMNYRGFTFPIWGFLANTDISYDPQKIDAQTCMAWMDNYRAGLSHQQQLRMFNQL
                                      D-----WETGIYYETW-----NVKASPEK-GAET---WFDSYDCS---KFVLRTFNKL 230
                                                                               KAPWSMDGWRLDVVHMLGEGGGARNNLQHIAGITQAAKQAQPEAFVFGEHFGDARQWLQA 387
                                                                                                                                                                                                                                                                               DIEVFRIQAPVWBFKYGDLLGHLKIMHDA--IGFRSTLTGK-NYTME---WYELFQLGNC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FKSKPVEKN----YAFEIPDVPEKSEYLEVKYSAEMPQLPQDLKGETFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYE----EIPLPIRNKTLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDSSHLPLVKGADBEQVFHFYWLDAYEDQYNQPGVVFLFGKVWIESAETHVSCCVMVKNI
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                                                                                                                                                                                                                                                                                                                                             Score 88; DB 4;
Pred. No. 0.7;
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Pred. No. 2.
                                                                                                                       ---NGTLVQVATIS------GNMFNQMAKWVKQ 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 115; Indels 107;
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                                                                                                                                                                                                                                                                                                                            95;
                                                                                                                                                                                                                                                                                                                                                                  Length 608;
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                                                                                                                                                                                                                                                                                                                            Indels 118;
                                                                                                                                                                                                    --FFEGIDDV--HWK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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CURRENT APPLICATION NUMBER: US/09/254,352B
CURRENT FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/JP98/03039
PRIOR FILING DATE: 1998-07-06
PRIOR APPLICATION NUMBER: JP 10-155847
PRIOR APPLICATION NUMBER: JP 10-155847
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 64
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S-09-134-000C-3624
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                 SEQ ID NO 19
LENGTH: 876
                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09254352B Patent No. 6365350
                                                                                                                                                                                                                                                                                                                                                                                                    -09-254-352B-19
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3624
LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCCCCUS FABCALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PELING DATE: 1997-08-15
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Patent No. 6617156
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD OF DNA SEQUENCING FILE REFERENCE: 024705-080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
                                                         SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                APPLICANT: HAYASHIZAKI,
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -MYYQATEPH 157
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RESULT 9
US-09-134-078-24
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Patent No. 6368844
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                                                                                                                                                                   APPLICATION NUMBER: 08/949,026
FILING DATE: 10-OCT-1997
APPLICATION NUMBER: 60/056,916
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGERRENCE/DOCKET NUMBER: 09010/024002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Bylina, E
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                  TELEFAX: 858/677-1465
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: T7 RNA polymerase
                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
FRAGMENT TYPE:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 858/677-1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM COMPONENTING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.5%;
Local Similarity 21.6%;
les 63; Conservative 2
                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/134,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                               TOPOLOGY:
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                                 linear
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GLYCOSIDASE ENZYMES
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -HHGLNSYNCS 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---PYNMDWRGRVYAVS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
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3SULT 10
3-09-079-030-217
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                                                                                                                                           3-09-079-030-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. boll-
Patent No. boll-
TOWERAL INFORMATION:
                                                                      Matches
                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                         TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 217:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MCMILLIAN, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/118-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Guevera, Jr., Juan G. APPLICANT: Hoogeveen, Ron C. APPLICANT: Moore, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/079,030 FILING DATE: Concurrently Herewith CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 -- IYALDISKDEVINWIFDIFSSIRKMGYRYFKID-----FIFAG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217, Application US/09079030
5. 6635623
                                  74 MEGDDDIEVFRLQAPVWEFKYGDLLG---HLKIMHDAIGFRSTLIGKNYIMEWYELFQLG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 FCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
                                                                                      Similarity
                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAKVIAENGFIPGIWTAPFSVSETSDVFNEHPDWVVKENGEPKMAYRNWNKK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YELF--QIGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWFDSYDCSK----FVLRTFNKLAEFGAEFKNIETNYTRIFLYSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YHYFLDLTWEETLKNLKLAKNFPFEVFQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Texas
                                                                                                                                                                                                            1056 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Arnold, White & Durkee P.O. Box 4433
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTLVQVATI-----SGNMFNQMAKW-VKQDNETGIYYETWNVKASPEKGAE 211
                                                                   4.3%; Score 83; DB 4; Length 1056
19.7%; Pred. No. 6.3;
Live 39; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.3%; Score 83; DB 4; Length 555.
22.1%; Pred. No. 2.3;
cive 32; Mismatches 68; Indels
 ---KWNFYYSPQSSPDKKLTIFKTELRVRESDEETQIKVNWEEEAASG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                ARAG: 003
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                                                                   66;
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                                                                 Gaps
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US-08-989-299-10
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                                                                                                                                                                          Matches
                                                                                                                                                                                                         Query Match
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Patent No. 619400.
Patent No. 619400.
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                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-025.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Arnold E., Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/989,299
FILING DATE: 11-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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 112
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                                                                                                                                       15 CWAL---
                                                                                                                                                                      l Similarity
77; Conser
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                                                                                                                                                                                                                                                                                                                              1310 amino acids
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                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   617-832-1000
                                                                                                                                                                                     4.3%;
19.7%;
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                                                                                                                                                                                                                                                                                                                                                                   10:
                                                                                                                                                                        61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Square
                                                                                                                                                                                        Score 83; DB 3; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version
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APPLICANT: Acton, Susan L.

APPLICANT: Robinson, Keith E.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 LSLLQIFDAVIVHKQFY-----LFYNFEYWFLPMKFPFIK 328
                                                                                                                                                                    61 KYTFCPTGS-----PIPVMEGDDDIE-VFRLQAPVWEFKYGDLLGHL-KIMHDAIGFR- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 LYSGEPTYLGNETSVFGPTGNKTLGLAIK-------RFYYPFKPHLPTKEFL 293
                                                                                                                                                                                                                                        CWSLDPDLNNILASSRSYAML-LFAWEGWHNAVGIPLK---PL-YQEFTALSN-EAYRQD 223
                                                                                                    --GFSDTGAYWRSWYDSPTFE--EDLERIYHQLEPL----YLNLHAYVRRVLHRRYGDRY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQEGQASFQGLKDNVFDGLVRVTQKFHMKVKHLIDSLIDFLNFPRFQFPGKPGIYTREEL 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN-YTRIF 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLT--SIKDNVP-----KATGVLYDYVNKYHWEHTGLTLREVSSKLRRNLQNNAEWVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTMF-IREVGTVLSQVYSKVHNGSEILFSYFQDLVITLPFELRK 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GAIRQIDDIDVRFQKAASGTTGTYQ------
-STLIGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHW 163 : | | :| :| 163
                                                                                                                                                                                                                                                                                                        ----ALLWIAVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDPYCQA 60
                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 8.8;
1; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1310;
                                                                                                                                                                                                                                                                                                                                                                                Indels 108;
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276

S-09-407-427-10

491 313 431

GENERAL INFORMATION:

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ORGANISM: Oryctolagus cuniculus $-09-407-427-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: MNI-132CP2
CURRENT APPLICATION NUMBER: US/09/407,427
CURRENT FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 08/989,299
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APPLICANT: Robison, Keith E.

TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
                                                                                                                                                                                                                                                                                                                                164 KENGTLYQVATISGNMFNQMAKWVKQDNETGIYYETW--NVKASPEKG-----AETWFD
                                                                                                                                                                                                                                                                                                                                                                                   276 INLRGPIPAHLIGNMWAQSWESIYDM-VVPFPD-KPNLDV----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 CWSLDPDLNNILASSRSYAML-LFAWEGWHNAVGIPLK---PL-YQEFTALSN-EAYRQD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 AIKRFYYPFKPHL-----PTKEFLLSLLQI-----FDAVIVHKQFYLF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 SYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFL-YSGEPTYLGNETSVFGPTGNKTLGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 KYTFCPTGS-----PIPVMEGDDDIE-VERLQAPVWEFKYGDLLGHL-KIMHDAIGFR- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 CWAL-----ALLWLAVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDPYCQA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GFSDTGAYWRSWYDSPTFE--EDLERIYHQLEPL----YLNLHAYVRRVLHRRYGDRY 275
                                                                          SVSTPAHLHKIGLLDHVTNDTESDINYLLKMALEKIAFLPFGYLVDQWRWGVFSGRTPSS
                                                                                                                                                                                                                                SYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFL-YSGEPTYLGNETSVFGPTGNKTLGL 274
                                                                                                                                                                                                                                                                                   --TSTMVQKGWNATHMFRVAEEFFTSLGLLPMPPEFWAESMLEKPEDGREVVCHASAW-D
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-YNFEYWFLPMKFPFIKITYEEIPLPIRNKT 342
                                                                                                                                                                             FYNRKDERIKQCTQVTMDQLSTVHHEMGHVQYYLQYKDQPVSLRRANPGFHEAIGDVLAL
                                                                                                                          AIKRFYYPFKPHL-----PTKEFLLSLLQI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ----STLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHW 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -YNFEYWFLPMKFPFIKITYEEIPLPIRNKT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.3%; Score 83; DB 4; Length 1310; 19.7%; Pred. No. 8.8; tive 61; Mismatches 145; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
                                                                                                                          FDAVIVHKQFYLF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 27: US-09-180-422B-27
RESULT 14
US-09-079-030-1
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US-09-180-422B-27
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: (Unknown)
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEPHONE: 7038164100
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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Patent No. 6444644
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity Matches 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BRUCKDORFER, KARL R
ETTELAIE, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3986 MDEDDDFS-----KWNFYYSPQSSPDKKLTIFKTELRVRESDEETQIKVNWEEEAASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22201
COMPUTER READABLE FORM:
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ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                              4039 LLT--SLKDNVP-----KATGVLYDYVNKYHWEHTGLTLREVSSKLRRNLQNNÄEWVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                              190
                                                                                                                                                                                                                                                     249 LYSGEPTYLGNETSVFGPTGNKTLGLAIK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 NCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG-TLVQVATISGNMFNQMAKWVKQ 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 MEGDDDIEVFRLQAPVWEFKYGDLLG---HLKIMHDAIGFRSTLTGKNYTMEWYELFQLG
                                                                                                                                                     LSLLQIFDAVIVHKQFY------LFYNFEYWFLPMKFPFIK 328
                                                                                                                                                                                                     TQEGQASFQGLKDNVFDGLVRVTQKFHMKVKHLIDSLIDFLNFPRFQFPGKPGIYTREEL
                                                                                                                                                                                                                                                                                                                                                           DNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN-YTRIF 248
                                                                                                CTMF-IREVGTVLSQVYSKVHNGSEILFSYFQDLVITLPFELRK
                                                                                                                                                                                                                                                                                                        ----GAIRQIDDIDVRFQKAASGTTGTYQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4536 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%; Score 83; DB 4; Length 4536; ilarity 19.7%; Pred. No. 63; Conservative 39; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM APOLIPOPROTEIN B-100
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                                                                                                     4232
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Best Loc Matches

77;

314

112

224

313

Query Match Best Local Similarity

SOFTWARE: 1

ENGTH: 1310

PRIOR FILING DATE: 1: NUMBER OF SEQ ID NOS:

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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                            Sequence 26565, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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APPLICATION NUMBER: US/09/079,030
FILING DATE: CONCURRENTLY Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MGMillian, Nabeela R.
REGISTRATION UNMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hoogeveen, Ron C. APPLICANT: Moore, Paul J.
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CITY: Houston
STATE: Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4536 amino acids
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                                                                                                                                                                                                                                                                                 294 LSLLQIFDAVIVHKQFY-----
                                                                                                                                                                                                                                                                                                                                                                     190 DNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN-YTRIF 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 NCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG-TLVQVATISGNMFNQMAKWVKQ 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512/474-7577
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                                                                                                                                                                                                                                                                                                                                                                                                                  --GAIRQIDDIDVREQKAASGTTGTYQ-------EWKDKAQNLYQELL 4129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 83; DB Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 123; Indels
                                                                                                                                                                                                                                                                               ---LFYNFEYWFLPMKFPFIK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66;
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Search completed: June 8, 2004, 14:09:15 Job time : 27.9111 secs
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26565
LENGTH: 322
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: US-60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                     Match 4.3%;
Local Similarity 25.0%;
                                                                                 277
                                                                                                                      128 QLGNCTFPHLRPEMDA------PFWCNQGAACFFEGIDD 160
                                                                                                                                                                                                                                                 186 ALVPGLREVGGVFSGDMWGNLYPRSGFLHQTDDY-----KTAAVIAQRAGDITTRVG
                                                                                                                                                               238 QLHVYLPMRAAPKDGYWPAGELKEGD-----
                                                                                                                                                                                                         84 RLQA-----
                                                                                                                                                                                                                                                                                        24 AVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDDDIEVF 83
                                                                                                                                                                                                                                                                                                                               41;
                                                                                 SINCAVEPNSGPKTQAVDGDYAWALWRPYSCCQRKGQIFLGSTD 320
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                         --PVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYEL---F 127
                                                                                                                                                                                                                                                                                                                               Score 82; DB 4; Length 322; Pred. No. 1.2; B; Mismatches 59; Indels
                                                                                                                                                               ----ASTGK-----WQELTPSL 276
                                                                                                                                                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                  Gaps
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.nimum DB seq length: 0
.ximum DB seq length: 20
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1927
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1368.675 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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: //cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*
:/cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
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:/cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
:/cgn2_6/ptcdata/2/pubpaa/US06_NEW_PUB.pep:*
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:/cgn2_6/ptcdata/2/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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91	91	91.5	91.5	93	94	95.5	96	97.5	472	886	1916	1916	1927	1927	Score
4.7	4.7	4.7	4.7	4.8	4.9	5.0	5.0	5.1	24.5	46.0	99.4	99.4	100.0	100.0	Match
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US-10-616-263-160	US-09-374-046A-160	US-10-425-114-57996	US-10-424~599-262855	US-10-282-122A-55615	US-10-282-122A-58749	US-10-408-765A-58	US-10-369-493-3172	US-10-369-493-12714	US-10-264-049-4034	US-09-864-761-39378	US-09-397-945-126	US-10-653-595-126	US-10-010-050A-2	US-09-122-383-2	ID III
Sequence 160, App	Sequence 160, App	Sequence 57996, A	Sequence 262855,	Sequence 55615, A	Sequence 58749, A	Sequence 58, Appl	Sequence 3172, Ap	Sequence 12714, A	Sequence 4034, Ap	Sequence 39378, A	Sequence 126, App	Sequence 126, App		Sequence 2, Appli	Description

ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/122,383A;
CURRENT FILING DATE: 1998-07-24

EARLIER APPLICATION NUMBER: 60/053,613

EARLIER FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 346

TYPE: PRT

ORGANISM: Homo sapien
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US-09-122-383-2
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                                                                                                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 346; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09122383A Patent No. US20020042093A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
  121 MEWYELFQLGNCTPPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMF
                       121 MEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMF 180
                                                                                 61 KYTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYT
                                                                                                       61 KYTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYT 120
                                                                                                                                                               1 MRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDFYCQA
                                                                                                                                                                                       1 MRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDPYCQA
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Pred. No. 6e-181;
n: Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/010,050A
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/122,383
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,613
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                ESULT 3 S-10-653-595-126
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ORGANISM: Homo
S-10-010-050A-2
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Best Local S
Matches 346
                                         Sequence 126, Application US/10653595 Publication No. US20040048304A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
                        APPLICANT: Ruben et.
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hes 346;
      OF INVENTION:
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    95 Human
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; OTHER INFORMATION:
US-10-653-595-126
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SOFTWARE: Pate
SEQ ID NO 126
FRIGHTH: 346
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR APPLICATION NUMBER: 60/080,312
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/078,578 PRIOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE LOCATION: (242) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
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DAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                    EXNYTXIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIF
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                                    DAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 346
                                                                                                                                                                                NQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNI
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Pred. No. 7.3e-180;
0; Mismatches 2;
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RESULT 4 US-09-397-945-126 Sequence 126, Application US/09397945 ; Publication No. US20030065139A1

INFORMATION:

USEFUL FOR

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SEQ ID NO 126
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (347)
OTHER INFORMATION:
-09-397-945-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE LOCATION: (246) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (242)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 34
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PRIOR FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/397,945
CURRENT FILING DATE: 1999-09-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/080,313
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APPLICATION NUMBER: 60/080,314
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                    ETNYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEELLSLLQIF 300
                                                                                    NQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNI
EXNYTXIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIF
                                                             NQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNI
                                                                                                                             MEWYELFOLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMF
                                                                                                                                                       MEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNWF
                                                                                                                                                                                              KYTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYT
                                                                                                                                                                                                                   KYTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLIGKNYT
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Pred. No. 7.3e
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ORGANISM: Homo sapiens FEATURE:
OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI OTHER INFORMATION: EXPRI
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR ETILING DATE: US 09/632,366
PRIOR PRIOR PRIOR NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 49117
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CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203 FILING DATE: 2001-01-29
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APPLICATION NUMBER: PCT/US01/00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00663
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00666
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o. US20020048763A1
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Then, Wensheng
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N: MAP TO AC001226.1

N: EXPRESSED IN PLACENTA, SIGNAL = 4.5

N: EXPRESSED IN BRAIN, SIGNAL = 6.3

N: EXPRESSED IN BOME WARROW, SIGNAL = 5.

N: EXPRESSED IN ADULT LIVER, SIGNAL = 5.

N: EXPRESSED IN LUNG, SIGNAL = 3.6

N: EXPRESSED IN HELA, SIGNAL = 3.9

N: EXPRESSED IN HEART, SIGNAL = 4.2

N: EXPRESSED IN FETAL LIVER, SIGNAL = 5.0

N: EXPRESSED IN FETAL LIVER, SIGNAL = 5.00e
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el, David K.
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APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, an FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
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   APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
FILE REFERENCE: 38-10 (52052)B
                                                                                                                                                                                       Sequence 12714, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                               -10-369-493-12714
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Publication No. US20040005579A1
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NAME/KEY: MISC FEATURE
LOCATION: (58)
TWENDMATION: Xaa
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-09-864-761-39378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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APPLICATION NUMBER: US/10/369,493
                                                                                                                                                                                                                                                                                                                                                                                                    258 GNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEY 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 346
                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244 YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 AKWYKQDNETGIYYETWNYKASPEKGAETWFDSYDCSKFYLRTFNKLAEFGAEFXNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                            88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                              WFLPMKFPFIKITYEEIPLPIRNKTLSGL 346
                                                                                                                                                                                                                                                                                                      WFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                                                                                                                                                                                                                                                                                                                GNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNXEY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 472; DB 15;
Pred. No. 1.6e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 886; DB 9; 1; Pred. No. 6.5e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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; TYPE: PRT ; ORGANISM: Neurospora crassa US-10-369-493-3172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Aspergillus nidulans US-10-369-493-12714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 12714
LENGTH: 328
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3172, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gre
APPLICANT: Slater, Ste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                 177
                       184 AK----
                                                                                                                                        118 KKĹTDĹ-ÍIGASÍGSEDLYRVSVTGIQNKSGVGAGPAELVKFIADWKKAFQGTAIANVPI 176
                                                                                                                                                                                  96 DLLGHLKIMHDAIG----FRSTLIG---
                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 WFDSYDCSKFVLRTFNKLAEFGAE----FKNIETNYTRIFLYSGEPTYLGNETSVFGPTG 268
                                                                                                                                                                                                                                                                59 QAK-YT----FCPTGSPIPVME----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 HPLGGLGFAR--WAFEVEMQEKE----LGVFFDTVIV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 TLVQVATISGNMFNQMA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
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                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hinkle, Gregory J.
Slater, Steven C.
Goldman, Barry S.
Chen, Xianfeng
                                                              GHVDTWDAWTNGTNKPVIDAVDWV---
                                                                                                                                                                                                                        AVRLYTNIQAYSQTSEPIEAFEAAIETNTKILLGVWASGTNTIEPEIKALQNGI--AKYG
                                                                                                                                                                                                                                                                                                 AGAAALLASGVSAEAYL-----GFNSGNTLPSREAKFKKDWVQEFTTAQNLKNSPGVFN 59
                                                                                                                                                                                                                                                                                                                                           AGAARGRASWCWALALLWLAVVPGWSRVSGIPSR----RHWPVPYKRF-DFRPKPDPYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLVSIGGFQSNHTRQVAAVARKLGLEVALVQEKWVDWDDKNGVYDKAGNIQLSRLMGADT 116
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                  ----RPEMDAPFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMFNQM 183
                                                                                                                                                                                                                                                                                                                                                                                                          5.0%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.1%;
-WYKQDNETGIYY--ETWNVKASPEKGAETWFDSYDCSKFVLRTFNKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---MSGFGIEHKLTLKNLE---EEIRARGGKPYYI-----PAGASD 154
                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                   Score 96; DB 1
Pred. No. 0.82;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 97.5; DB 15;
Pred. No. 0.69;
9; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 290;
                                                            |:|: : ||| : :|::
-GVDEYPYYENGKGNNIEN-SGYLFDRA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KWVKQDNETGIYYETWNVKASPEKGAET 212
                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                              -GDDDI--EVFRLOAPVWEFKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
                                                                                                                                                                                    -KNYTMEWYELFQ---LGNCTF 134
                                                                                                                                                                                                                                                                                                                                                                                   Indels 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLANTS FOR PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                              95
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SULT 10
-10-282-122A-58749
                                                                                                                                       APPLICANT: Wang,
APPLICANT: Zamud
APPLICANT: Malon
APPLICANT: Hasel
                                                                                                                                                                                                                       Sequence 58749, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :SULT 9
:-10-408-765A-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 58, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 58
                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ghosh, APPLICANT: Fahy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                       APPLICANT
                                        APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                       476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 TSAPSPAVGTVGMDMDEDDDFS-----KWNFYYSPQSSPDKKLTIFKTELRVRESDEE 324
                                                                                                                                                                                                                                                                                                                                                                                                         280 YYPFKPHLPTKEFLLSLLQIFDAVIVHKQFY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 TGSPIPV-----MEGDDDIEVFRLQAPVWEFKYGDLLG---HLKIMHDAIGFRSTLTG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang, Bing
Gibson, Bradford W.
Taylor, Steven W.
Glenn, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFKNIETN-YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGNMENQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOIKVNWEEEAASGLLT--SLKDNVP-----KATGVLYDYVNKYHWEHTGLTLREVSSK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG-TLVQVATI 175
                                                                                                                                                                                                                                                                                                                                                                     QFPGKPGIYTREELCTMF-IREVGTVLSQVYSKVHNGSEILFSYFQDLVITLPFELRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWKDKAQNLYQELLTQEGQASFQGLKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPRF 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRRNLQDHAEWVYQ----GAIREIDDIDERFQKGASGTTGTYQ------ 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YDAIEGAVGGKPIWV---TETGWPYVGQTWDQAAATIKNQQYYWQEVGCRKL----FGKV 279
                                                                                                 Ohlsen, Kari
Zyskind, Judith
                                                                                                                                       Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fahy, Eoin D.
  Yamamoto, I
Forsyth, R
                                        Carr, Grant
                                                             Trawick, John
                                                                                Wall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                  Liangsu
                                                                              Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soumitra S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
                       Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.0%; Score 95.5; DB 16;
20.5%; Pred. No. 3.8;
tive 39; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                           ----LEYNFEYWELPMKFPFIK 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 836;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -RF 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                 US-10-282-122A-55615

Sequence 55615, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58749
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                                                                                APPLICANT:
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
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                                                                                                                                                            APPLICANT: Wang, Liangsu
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PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
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                       APPLICANT:
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62; Conserv
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Wall, Daniel
Trawick, John
Carr, Grant
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                                                           Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                      Zamudio, Carlo
Malone, Cheryl
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Gaps

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YNFEYW-FLPMK 323 -SSGSAKINVSQ 634

Length 1238; Indels 96;

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S-10-424-599-262855
S-quence 262855, Application US/10424599
Publication No. US20040031072A1
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Matches
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                                                                                 GENERAL INFORMATION:
APPLICANT: La Rosa Thomas
APPLICANT: Kovalic David
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SEQ ID NO 55615
LENGTH: 478
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
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                                                                    APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes
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APPLICATION NUMBER: 60/267,636
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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APPLICATION NUMBER: 60/257,931
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FILING DATE: 2000-09-06
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                                                                 Zhou Yihua
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Pred. No.
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Mismatches
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US-10-425-114-57996
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SEQ ID NO 57996
LENGTH: 350
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 262855
LENGTH: 347
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Publication No. US20040034888A1
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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua APPLICANT: Kovalic, Dav
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Zea mays FEATURE:
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                                                                                                                                                                                        4 GAGAARGRASWCWALALLWLAVVPG-----WSRVSGIPSRRHWPVPYKR---FDFRPK 53
                                                                                                                                                                                                                                                 Similarity
- VGVFS--TGNNFKRRMALRRTWMQYEAVRSGDVVVRFFTGLHKNEQVNMELW----REAQ 159
                                                                         SEPWLVAEVMFSGDLELLSFLANELPVSEDIDMENVAVLKAPPLPKKQTFLL-
                                                                                                             PDPYCQAKYTECP----
                                                                                                                                                  GHGQLSGRFS-----
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                              AIGERSTLTGKNY-----TMEWYELFQLGNC----TFPHLRPEMDAPFWCNQGAAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMDHQPKTW--EFQLNSGIQTIAVIAVREGLVQLGSFNKI----AEDLNFVVSIQRKF--
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23.9%;
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; Pred. No. 2.9;
25; Mismatches
                                                                                                           --TGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHD 106
                                                                                                                                                    ---IVEGEPFTVTLWAGVEGF----HMTVNGRHETSFAYRER
                                                                                                                                                                                                                                               Score 91.5;
Pred. No. 2
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Matches
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APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikii
APPLICANT: Wong, Gordon G.
APPLICANT: Wong, Gordon G.
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLB OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6075-83A
CURRENT APPLICATION NUMBER: US/09/374,046A
CURRENT APPLICATION NUMBER: US/09/374,046A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 160, Application US/09374046A Publication No. US20030096951A1
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SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: LaVallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Homo sapiens
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TFINTVFYNTDLFEYKFVNSR--LINSTFLHNKEGCPLDV 587
                                                                                                                               ----GPTGNKTLGLAIKREYYPFKP-----HLPTKEFLLSLLQ--IFDAVIVHKQFY--- 310
                                                                                                                                                                                                                         LRTENKLAEFGAEFKNIETN----YTRIFLYSGEPTYL-----GNETSVF--
                                                                                     ERVEHVTFNFTLENQIHRGGQYFNDKFIGLRLKSVSFEDSLFEECYFEDVTSSNTFFRNC 549
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                                            ---LFYN---FEYWFLPMKFPFIKITY----EEIPLPI 338
                                                                                                                                                                            --FGPEYRRITLMMMGVWFTMSFSYYGLTVWFPDMIRHLQAVDYASRTKVFPG 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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SEQ ID NO 160
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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APPLICANT: Genetics Institute, Inc.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000103.5
CURRENT APPLICATION NUMBER: US/10/616,263
CURRENT FILLING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 240
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                                                  TFINTVFYNTDLFEYKFVNSR--LINSTFLHNKEGCPLDV 587
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Merberg, Maurice
Michae
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Steininger II, Robert J.
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Wong, Gordon G.
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                                                                                    ---LFYN---FEYWFLPMKFPFIKITY----EEIPLPI 338
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2004, 14:11:56
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Search completed: June Job time: 72.1222 secs 8

-10-616-263-160 Sequence 160, Application US/10616263 Publication No. US20040038276A1

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Ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1331.883 Million cell updates/sec
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A;Map position: 5
A;Introns: 102/3; 157/2; 288/2; 439/3; 542/1; 591/3; 798/3; 835/3; 1139/1; 1204/3; 1325/]
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C1Species: Caenorhabditis elegans
C1Species: Caenorhabditis elegans
C1Species: Coet-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18995
R,Steward, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19057
A;Reference number: Z19057
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-3036 <WIL>
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T18995
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Best Local Similarity
Matches 103; Conserv
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                                               GTGNEAVIAQRVFDFDDWNTFTRAEWTPFYVSNDLSINFWWNPWRDGQLANATYLEPGVH
                                                                                                                                                   MEKNLICERNRFFFNWG----HWMIKLDATSQYLRQIDVPSYVQYNYIEK-NRFINQRGD
                                                                                                                                                                          MDAPFWCNQGAACFFEGIDDVHW--KENGT---LVQVATISGNMFNQMAKWVKQDNETGI 195
                                                                                                                                                                                                    SFWLTENRFERNSEFKILLDGYYAFANISSNNFTLN-----TAPKQFGMVELR-G 1607
                                                                                                                                                                                                                                                   NCSVTDNSGPIIESHRDLYASANVFHW--ILWSNTFANNSRSGIAVALPDTYDLLAKQTH 1558
                                                                                                                                                                                                                           -----GHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFP-----HLRPE 140
                                                                                                                                                                                                                                                                               -CP-TGSPIPVMEGDDDI----EVFRLQAPVWEFKYG---
                                                                                                                                                                                                                                                                                                      GRLSNRWNNEKIWLOKV-NFTRNSEAVMWLHSPQHAVVP-----GTPIABITYHFD 1500
                                                                                                                                                                                                                                                                                                                               GRASWCWALALLWLAVVPGWSR----VSGIPSRRHWPVPYKRFDFRPKPDPYCQAKYTF-
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PRSYALGVFGSQKVEVHFNRFFNELIDFELVSGAKYSDVFETMNTTHNWW 1717
                         KTLGLAIKRF-----YYPFKPHLPTKEFLL---SLLQIFDAVIVH----K 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone C06B8
                                                                           -RIFLYSG-----EPTYLGNETSV---
                                                                                                                                                                                                                                                                                                                                                                       5.3%; Score 101.5; I 22.2%; Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         653
1086
4563
403
509
704
386
456
477
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640
984
228
552
620
                                                                                                                                                                                                                                                                                                                                                            52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAB03852.1; GSPDB:GN00023; CESP:C06B8.
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A36709
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T27008
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H69399
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                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                         143;
                                                                                                                                                                                                                                                                                                                                                                                 Length 3036;
                                                                                                                                                                                                                                                                                                                                                         Indels 165;
                                                                           ----FGPTGN-----
                                                                                                                                                                                                                                                                              -----DLL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable glycopori
alpha-amylase (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beta-xylosidase (1 hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uromodulin precurs
cellulose 1,4-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fosmidomycin resis
cyprosin (EC 3.4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical prote apolipoprotein B-1
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Query Match

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Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon: Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I nsen, N.F.; Hughes, B.; Huizar, L.

ature 408, 816-820, 2000

Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, J.; Lin, X.; Liu, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Waiti, R.; Kim, izzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

izzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

jauthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallor, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

jTitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

jAccession: A98816
                                                       Molecule type: DNA Residues: 1-362 <KAL>
                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                       Kalicki, J.; Smith, A.; Gibson, A.
bmitted to the EMBL Data Library, February 1999
Description: The sequence of C. elegans cosmid Y25ClA.
                                                                                                                                                                                                                                                                             pothetical protein Y25C1A.7a - Caenorhabditis elegans
Species: Caenorhabditis elegans
Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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           Experimental source:
                                                                                                                                                                  Reference number: Z21437
                                                                                                                                         Accession: T33904
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                                                                                                                                                                                                                                                                     Accession: T33904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: DNA
Residues: 1-359 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9K20.25 [imported] - Arabidopsis thaliana
;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: A9681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 EWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFF---EGIDDVHWKENGTLVQVAT---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 MWVSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 YRWQPTGCDIPRFNGRDFLTRFKGKKILF---VGDSLSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFKIALTTWSKWIDHNIDPSKTRVFYQGVSPVHLNGGE---WGKPGKTCLGETVPVQGPS 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPFKPH 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFGAEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLILKLDSISRGNOWLGSDVAIFNTFHWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTM 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RILVLGNLVARGEYW-QPIRFKPINVTEYMQYKGEIPTEYRKK 1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QEYLFYNF----EYWFLPMKFPFIKIT----YE-EIPLPIRNK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.0%; Score 95.5; I ilarity 21.5%; Pred. No. 2; Conservative 39; Mismatches
EMBL:AF125459; PIDN:AAD12838.1; GSI
De: strain Bristol N2; clone Y25CIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE005173; NID:g3834323; PIDN:AAC83039.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SCMLHAAVPNAKYTFQLNKGLSTFTIPEYGI-SVNFLKNGFLVDLVSDKTR 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KNIETNYTRIFLYSGEPTYL-GNETSVFGPTGNKTLG--LAIKRFY 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---SHTGRAKTW-DYFQTGDKIVKEMNRME
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                      GSPDB:GN00020; CESP:Y25ClA.7a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
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RESULT T19604

hypothetical protein C31C9.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
A;Residues: 1-1238 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fras A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID: 97394467; PMID: 9252185

A;Accession: A64596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein HP0609 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
G;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: A64596
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
A64596
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A; Introns: 7/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:Y25C1A.7a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Best Local :
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mes 48; Conserv
                                          324
                                                                                    635
                                                                                                                              277
                                                                                                                                                                                                                                                          556
                                                                                                                                                               589 LNFVGATEINIA--GATFKNLKTTSQNSYMTFMALGD-----
                                                                                                                                                                                                   220 SKFYLRTENKLABEGABEKNIET ~-- NYTRIFLYSGBPTYLGNETSVEGPTGNKTLGLAI 276
                                                                                                                                                                                                                                                                                                                                            513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 IMHDAIGFRSTLTGKNYTMEWYELF------QLGNCTFPHLR------
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                                                                                  SDFYDWTGGGYDFTGN--
                                   FPFI-KITYBEIPLPIRNKTLSG 345
                                                                                                                                                                                                                                                                                       ENGTLVQVAT----ISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDC
                                                                                                                     KRFY-----YPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLF-----YNFEYW-FLPMK 323
                                                                                                                                                                                                                                                                                                                                                                         FRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCN-----QGAACFFEGIDDVHWK 164
FKFQGKTTIEKSVLSDASYTFDG
                                                                                                                                                                                                                                                      KTGYITGTFTADRVYITGNMM----
                                                                                                                                                                                                                                                                                                                                    FTQTYGGKNSALVF-----NATTP-----WANGSIPKSNSTVRFGGYEGVNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KASPEKGAE----TWEDSYDCS--KEVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFDDSQSTTSTRKGNFFSFEYYQQFFDVETDQVIKRLLNSVIPTHRNYIQDFLQPIPDLW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FC-NLSHGFLTNGNLKTGSFSEQKMNFYTSFITSASTLIFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.9%; Score 94; DB
21.7%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                        7; Score 94; DB 2;
7; Pred. No. 13;
28; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27; Mismatches
                                                                             ---GVFDSVNFNKAYYKFQGTENSYNFKNTNFLAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLVFAIGIFGN----LAOFIENDGAKGTYGSDFRM 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 362
                                                                                                                                                                                                                                                                                                                                                                                                                        77;
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.;Molecule type: DNA
.;Molecule type: DNA
.;Residues: 1-1327 <HAY>
.;Cross-references: GB:BA000007; PIDN:BAB33785.1; PID:g13359819; GSPDB:GN00154
.;Cross-references: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          asawara, N.; Yasunaga, Tasawara, N.; Yasunaga, N.; Yasunaga, Tasawara, N.; Yasunaga, N
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;Reference number: A99629; MUID:21156231; PMID:11258796
;Accession: B90674
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;Species: Escherichia coli
;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
;Accession: B90674
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Residues: 1-561 <WIL>
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                                                             FRSTLTG--KNYTM---
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Kasunaga, T.; Kuhara, S.;
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20.7%; Pred. No. 5.7;
ative 41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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                                                                    -LFQLGNCTFPHLRPEMDAPFW 146
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A;Residues: 1-1349 <STO>
A;Cross-references: GB:AE005174; NID:g12513130; PIDN:AAG54657.1; GSPDB:GN00145;
A;Experimental source: strain 0157:H7, substrain EDL933
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable beta-barrel outes membrane protein 20402 (imported) - Escherichia
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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                                                                                                                  Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70316
                                                                                                                                                                                                                                        C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
C;Accession: F70316
                                                      A; Molecule type: DNA
A; Residues: 1-502 < A(
                                                                                        A;Status: preliminary; nucleic acid sequence
                A; Experimental source: strain
                                   A;Cross-references: GB:AE000677; NID:g2982900; PIDN:AAC06534.1;
                                                                                                                                                                                                                   R;Deckert, G.; Warren, P.V.; Gaasterland, T.;
                                                                                                                                                                                                                                                                                               conserved hypothetical protein aq 175 - Aquifex aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                         1-502 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQNGSDRWHVGVMAGYGNSDSKTISSRTGYRAKASVNGYSTGLYATWYADDESRNGAYLD 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNQGAACFFEGIDDVHWKENGTLVQ------VATISGNMFNQMAKWVKQD-NETGIYYE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTDMVTGEQKQTTMWMRHEGGHNKWRDGSGQLKTQSNRYVLQLGG------DVAQW 1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPNPNPTPTPGPDLNVDNDL---RPEA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKI-------MHDAIG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MRRGAGAARGRASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDPYCQA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWNVKASPEKGAETWFD-
                                                                                                                                                                                                                                                                                                                                                                                                         SW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWNVKASPEKGAETWFD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQNGSDRWHVGVMAGYGNSDSKTISSRTGYRAKASVNGYSTGLYATWYADDESRNGAYLD 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNQGAACFFEGIDDVHWKENGTLVQ-----VATISGNMFNQMAKWVKQD-NETGIYYE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRSTLTG--KNYTM-----EWYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -AQYSWFDNTVKGDDLQSESYKSKGFTASLEAGYKHKLAEF 1184
                                                                                                                                                                                                                                                                                                                                                                                                         -AQYSWFDNTVKGDDLQSESYKSKGFTASLEAGYKHKLAEF 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 93; DB
Pred. No. 17;
32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -NWYLTSGSDSPELQPEP----DPMPNPEPNPNP 1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYDCSKEVLRT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYDCSKFVLRT----FNKLAEF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z0402 [imported]
                                                                                                   not
                                                                                                                                                                                                                       Young,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GSYIANLAAANTMFTTRLHERLGNTY
                                                                                                   shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- LFQLGNCTFPHLRPEMDAPFW 146
                                                                                                                                                                                                                           W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FNKLAEF
                                                                                                     translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli 0157:H7
                                                                                                                                                                                                                           Lenox,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Escherichia coli (strain (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.D.; Rose, Potamousis,
                                          PID:g2982916; GB:AE000657
                                                                                                                                                                Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                                                           A.L.; Graham,
                                                                                                         not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.J.; Mayhew,
K.; Apodaca,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UWGP: 204(
                                                                                                                                                                                                                                D.E.;
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Spring

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liLennard, N.

nbmitted to the EMBL Data Library, January 1997

NReference number: Z19461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: probable 60K inner membrane protein; stage III sporulation F;293-486/Domain: stage III sporulation protein homology <SPOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Experimental source: clone F33E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wpothetical protein F33E2.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-291 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: CESP:F33E2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Date: 15-Oct-1999; Accession: T21702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position:
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         316
                                                                                                                         177
                                                                                                                                                             210
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                                                                                                                                                                                                                                      152
                                                                                                                                                                                                                                                                                                                112
                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                            57 YCQAKYTFCP----TGSPIPVMBGDDDIEVFRL-QAPVWBFKYGDLLGHLKIMHDAIGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314
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                                                                                                                                                                                                                                                                                                                                                                                                                                57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
     EYWFLPMKFPFIKITYEE
                                                                       KTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFY----
                                                                                                                                             AETWFDSYDC$KFVLRTFNKLAEFGAEFKNI FINYTRI FLYSGEPTYLGNETSVFGPTGN
                                                                                                                                                                                                                       ACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVK--QDNETGIYYETWNVKASPEKG
                                                                                                                                                                                                                                                            DTDIPANYIAVSMALPNFKIGQNCHDFQPLDWYKNIK-GYFTYKKITEQVQAAVFNDEAG
                                                                                                                                                                                                                                                                                                                                        YPEARYPTIPKILKKTADFQKLEGSKORIAFTLSQEPIADKKCTEMIKNVLLEQ----FQ
                                                                                                                                                                                                 NOFLAGV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LŚILVLTFIVRIFLFPLGYKSVVSMQKLQE--LAPKMEKIKQKYKDDPVKMQEEMM 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSLL-----QIEDAVIVHKQEYLEYNEEYWELEWKEPFIKITYEEIPLPIRNKTL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRIFLYSGEPT-YLG-----NETSVFGPTGNKTLGLAIK---RFYYPFKPHLPTKEFL 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNCTFPHIRPE-MDAPFWCNOGA----ACFFEGIDDVHWKENGTIVQVATISGNWFNQMA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLEIFTGNPDLDQ-KLNFGEYEIKEGK--NSVELIHKELKVKKILSYKNGAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----DDLKGINEFEGNIEFGGEESRYFFKGAKDYQKHIVYK----VKLGDKFVSLSI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNY 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----HLSVEGLKPPFWVFVGSPPDDEAFYTHVGPV-LKINGEVVRLDV------
                                                                                                               --FPLNSKSRFDTKAFKKFARYG---RYCETEGCRVLVWVGKA
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLYDGEKTIYLGAKDYARLRELGLVDTLDWGTLKIIVKPLFLFLYWIYEH--TGSWV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                          4.7%; Score 91;
17.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%;
                                                                                                                                                                                     --CYYATPAG-----KWVAKLQTEQTLLRFEF--QKAEP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                    -----TMEWYELFQLGNCTFPHLRPEMDAPFWCNQGA 151
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGQIVHLNYHPVYCMQWTKGCAECAKDHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                        92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSPDB:GN00019; CESP:F33E2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 291;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                         -NF 315
                                                                                                                                                 269
                                                                                                                                                                                     175
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                                                                                                                                                                                                                                                                13)
                                                                                                             214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166
                                                                                                                                                 A;Note: also has alpha-amylase activity
C;Superfamily: neopullulanase; alpha-amylase core homology
C;Keywords: 9lycosidase; hydrolase; polysaccharide degradation
F;293-424/Domain: alpha-amylase core homology <AMY>
F;329,354,421/Active site: Glu, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                      C;Accession: JC1486
R;Tonozuka, T.; Ohtsuka, M.; Mogi, S.; Sakai, H.; Ohta, T.; Sakano, Y. Biosci. Biotechnol. Biochem. 57, 395-401, 1993
A;Title: A neopullulanase-type alpha-amylase gene from Thermoactinomyces A;Reference number: JC1486; MUID:93222535; PMID:7763540
             먑
                                           Š
                                                                                                                                                                                                                                                      A;Description: hydrolysis of alpha-(1->4)-glucosidic linkages A;Pathway: pullulan degradation
                                                                                                                                                                                                                                                                                                    A;Residues: 1-585 <TON>
A;Cross-references: GB:D13178; NID:g391625; PIDN:BAA02473.1; PID:g398125
                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-585 < To
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neopullulanase (EC 3.2.1.135) - Thermoactinomyces vulgaris
N;Alternate names: alpha-amylase II
C;Species: Thermoactinomyces vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 닭
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Col
Nature 402, 769-777, 1999
A;Tille: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: AT4g04460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-508 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
C;Accession: D85056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable aspartic proteinase [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 31-Dec-1993 #sequence_revision 18-Aug-1995 #text_change 16-Jun-2000
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                  Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Genetics:
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                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 YFHSKYKASQSSYRKNGKÞASIRYGTGAISGYFSNDDVKVGDIVVKEQEFIEATSEPGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 YCQAKY-----TFCPTGSPIPVMEG------DDDIEVFRLQAPVWEF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244
                                                                                                       Similarity
IKIILDAVFNHAGDQFFAFRDVLQKGEQSRYKDWFFIEDFPVSKTSRTNYETFAVQVPAM 293
                                                 LKIMHDAI --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRNPKDPEGGEIVFGGVDPKHFKGEHTFVPV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFLLAKFDGILG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-----QGAACFFEGIDDVHWKENGTLVQV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----KYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYMWIAPEEPVVQKSKEE
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:NC_001268; NID:g7267203; PIDN:CAB77914.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.7%;
                                                                                                   21.5%;
                                         ----GFRSTLT--GKNYTMEW---
                                                                                                                       4.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LGFKEISVG-NSTPVWYNMVEKG---
                                                                                 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
                                                                                                   Score 90; DB
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 91; DB
Pred. No. 7.5;
                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homology
                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                             ; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                 Length 585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change 17-May-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                             Indels
                                                                                                                                                                                                                                                                  of pullulan
                                       YELFQLGNCTF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LVKEPIFSFWL
                                                                             96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50;
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                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :Gene: CESP:Y75B8A.22
:Introns: 28/1; 79/2; 634/3; 996/1; 1134/1; 1296/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Molecule type: DNA;Residues: 1-1353 <WIL>;Residues: 1-1353 <WIL>;Cross-references: EMBL;AL033514; NID:e1343251; PIDN:CAA22106.1; CESP:Y75B8A.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Barlow, K.

Dmitted to the EMBL Data Library, November 1998;Reference number: Z20361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: T27404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Experimental source: clone Y75B8A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: T27404
phosphatase (EC 3.1.3.2) purple 1, pecies: Ipomoea batatas (sweet potato)
                                                                                           915
                                                                                                                                                                                                              821
                                                                                                                                                                                                                                                                                                       155
                                                                                                                                                                                                                                                                                                                                                                                     667 AESCKTCDEDPAYKKYDKMDATALQS-LWE-QSTDTLARI-LSHELPESEST-SPVNWQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               458
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                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 RVSGIP-----SRRHWPVPYKR--FDFRPKPDPYCQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73;
                                                                                        SRLYELYQFGFHLLKKFFSKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                   FYLEYNFEYWFLPMKFPFIKIT 330
                                                                                                                                                                         GNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVH---
                                                                                                                                                                                                           EEEEVPAWKVEEIDFQFDSYVC
                                                                                                                                                                                                                                                                                            FEGIDDVHWKENGTLVQVATISGNM----FNQMAKWVK-----QDNETGIYYETWNVKAS
                                                                                                                                                                                                                                                                                                                                                                                                                 YTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLIGHLKIMHDAIGFRSTLTGKNYTM 121
                                                                                                                                                                                                                                                                                                                                                                                                                                              RSRGFPAAVGLYHASRALWPESFKRGLTDFQDSPGEEDQLQELEQLLKADMKKVAKDLKK 666
                                                                                                                                                                                                                                          PEKGAETW
                                                                                                                                                                                                                                                                                                                                                               EWYELFQLGNCTFPHLRPEMDAPF-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE-TW-~FDSYDCSKFVLRTENKLAEFGAEFKNIETNYTRI----FLYSGEP-TYLGNE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISGNMFNQMAKWVKQDNETGI------YYETWNVKAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIVGEIWHDASGWLMGDQFDSVMNYLFRESVIRFFATGEIHAERFDAELTRARMLYPEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQGLWNLLDSHDTERFLTSCGGNEAKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKLRTENPEVKEYLFDVARFWMEQG----IDGWRLDVANEVDHAFWREFRRLVKSLNPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHLR---PEMD-----APFWCNQGAACFFEG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267
                                                                                                                                          -NQALVKMLHRIAFDLK--LPIKLYQVSLFQVFSKVNEHFTHLSKDLRKS 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.6%;
                                                                                                                                                                                                                                                                -GVEEEIAELKAILEADLHEVAREMKVAEDRAEDPDEEDPAEPYDSEQE
                                                                                                                                                                                                                                                                                                                             -ITPDVQQKFAMLAIQRALRARDLPAAVGLYHTSRKLWPGDEAIFG
                                                                                                                                                                                                                                  FDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 89; DB
Pred. No. 38;
                                                                                        936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
             precursor [similarity] -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124;
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                                                                                                                                                                                                       -KFSNVDVLKWYVFLLN---DFS 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RLAVLFOMTYLGTPLIYYGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134;
            sweet potato
                                                                                                                                                                                                                                                                                                                                                         WCNQGAACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kudoh Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyru A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: E72616
                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein APE1390 - Aeropyrum pernix (strain K1) C;Species: Aeropyrum pernix (c;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_cbc;Accession: E72616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-752 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: kidney bean purple acid phosphatase; phosphoesterase core homology C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change C;Accession: T51094
C;Accession: T51094
R;Durmus, A.; Eicken, C.; Spener, F.; Krebs, B.
Biochim. Biophys. Acta 1434, 202-209, 1999
A;Title: Cloning and comparative protein modeling of two purple A;Reference number: 225292; MUJD:20028255; PMID:10556574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: pap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: EMBL: AJ006224; PIDN: CAA06921.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-465 <DUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T51094
                                                                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80387.1; PID:d1044173; PID:g5109;Experimental source: strain Kl
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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         248
                                                    132
                                                                                                                                                                                    180 ILWLGQYKVVFVYWSWVKGL---YYHPTLDIRFDLISE-DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 HVPYKASGSTETFWYSIKRASAYIIVLSSYSAYGKYTPQYKWLEEELP--KVNRTETP 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                280
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                                                                                                                                           76
                                                                                                                                                                                                                   20 LLWL----AVVPGWSRVSGIDSRRHWPVPYKRFDFRPKDDPYCQAKYTFCPTGSPIPVME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 VHWKENGTLVQVATISGNM-----FNQMAKWVKQ-----DNETGIYYET---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                            67;
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                                                                                                                                                                                                                                                                                                       Similarity
                                           CTFPHLRPEMDAP-----FWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMFNQMA-K 185
                                                                                                                                 GDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLIGKN----YTMEWYELFQLGN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYPFKPHLPTKEFLLSLLQIFDAVİVHKQF--YLFYNFEYWFLPMKFPFIKITYEEIP 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DLSYADNYPNHDNVRWDTWGRFVERSTAYQFWIWTAGNHEIDFAPEIGETKPFKPFTKRY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIE--TNYTR-----IFLYSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYWSENSQHKKVA--KGNIRTYTYFNYTSGYIHHCTIRNLEYNTKYYYEVGIGNTTRSFW 144
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 31;
  -PAADYETFGWHIWHNIGQTLV-
                                                                                                  -NAPVVD-
                                                                                                                                                                                                                                                                   4.6%; Scu
19.7%; Pre
rative 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.68;
                                                                                                                                                                                                                                                                        Score 88.5; DB 2;
Pred. No. 20;
4; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 88.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VPYTFGLIGDLGQSFDSNRTLTHYERNPIKGQAVLFVG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-Aug-1999 #text_change 20-Aug-1999
                                                                                        -LGFGGYSNGPNTWVDVTFGWPDTFD---
  -TFWKDETT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
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                                                                                                                                                                                                                                                                                                                     Length 752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 465;
                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                          133;
-ELTPELAVA
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286 WAHNEDSTEWYFVIRGGVKAFDNWNNKTYDDVTANDVLFTIRWIARUSLDESWNWITEE 342 237 FKNIETNYTRIFL	286 WAHNEDSTEWYFVIRGGVKAFDNWNNKTYDVTAVDULTTIWRIAFLSLDPSWMITEF 237 FKNIETNYTRIFL

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SUMMARIES

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL; APO6827; AAC27614.1; EMBL; APO6827; AAC27614.1; Genew; HGNC:2076; CINS.	Hum. Mol. Genet. 11:885-891(2002)!- FUNCTION: Not known!- SUBCELLULAR LOCATION: Lysosomal!- SUBCELLULAR LOCATION: Lysosomal!- TISSUE SPECIFICITY: Ubiquitous!- DISEASE: Defects in CLN5 are the cause of Finnish variant late- infantile neuronal ceroid lipofuscinosis (VLINCL) [MIN:256731]; also known as ceroid lipofuscinosis neuronal 5 (CLN5). VLINCL is a fatal childhood neurodegenerative disease characterized by progressive visual and mental decline, montor disturbance, epilepsy and behavioral changes. The first symptom is motor clumsiness, followed by progressive visual failure, mental and motor deterioration and later by myoclonia and seizures!- DATABASE: NAME=NCI CLN5; NOTE=Neural Ceroid Lipofuscinoses mutation db; WMW#"http://www.ucl.ac.uk/ncl/CLN5.html".	SEQUENCE FROM N.A., VARIANT VLINCL ASN-279, AND VARIANT ARG-368. TISSUB=Fetal brain; MEDLINE=98324783; PubMed=9662406; Savukoski M., Klockars T., Holmberg V., Santavuori P., Lander E.S., Peltonen L.; "CLNS, a novel gene encoding a putative transmembrane protein mutated in Finnish variant late infantile neuronal ceroid lipofuscinosis."; Nat. Genet. 19:286-288(1998). [2] SUBCELLULAR LOCATION, AND GLYCOSYLATION. MEDLINE=21968572; PubMed=11971870; IEOSOMOPDI J., Vesa J., Jalanko A., Peltonen L.; "Lysosomal localization of the neuronal ceroid lipofuscinosis CLN5"	HIMMAN STANDARD; PRT; 407 AA. CLN5_HUMAN STANDARD; PRT; 407 AA. 075503; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Ceroid-lipofuscinosis neuronal protein 5 (CLN5 protein). CLN5. CLN5. Homo sapiens (Human). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1]

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115-MAR-2004 (Rel
Inner membrane poxaa OR AQ_175.
                                                                     Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex
                    Nature 392:353-358(1998).
                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=VF5;
                                                                                                                                                                                                                                         Aquifex aeolicus.
Bacteria; Aquificae; Aquificales;
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQUAE
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CARBOHYD
                                                                                                                                                             MEDLINE=98196666; PubMed=9537320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; 256731; -.
; GO:0016021;
; GO:0008151;
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(Rel. 43, Last sequence update)
(Rel. 43, Last annotation update)
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P:cell growth and/or maintenance; TAS.
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Probably plays an
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Pred. No. 2.8e-157;
Mismatches 0;
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  of integral membrane proteins essential role in the
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SEQUENCE

FROM N.A

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ESUL.

PTPY MOUSE

ID PTPY MOUSE

ID PTPY MOUSE

ID PTPY MOUSE

ID STANDAM.

AC P70289;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 43, Last sequence update)

PT Receptor-type protein-tyrosine phosphatase V precursor (EC Receptor-type protein-tyrosine phosphatase) (ES cell protein-tyrosine phosphatase)

Note that the standard protein in the standard phosphatase (ES cell protein in the standard phosphatase) (ES cell protein in the standard phosphatase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 63
                                   Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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               NCBI_TaxID=10090;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP; MF_01810; -; 1.
InterPro; IPR001708; 60kDa_innermeb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).
-!- SIMILARITY: Belongs to the OXA1/oxaA family.
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SUBUNIT: Specifically interacts with transmembrane segments complex substitutions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                   LSLL-----QIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTL
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Pred. No.
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                                   Craniata; Vertebrata; Sciurognathi; Muridae;
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InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_pp.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
PRINTS; PR00700; PRTYPHPHTASE.
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SMART; SM00194; PTPC; 1.

PROSITE; PS00383; TYR PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR PHOSPHATASE PTP; 2.
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MEDININE=97109513; PubMed=8951793;
Lee K., Nichols J., Smith A.;
"Identification of a developmentally regulated protein tyrosine phosphatase in embryonic stem cells that is a marker of pluripotential epiblast and early mesoderm.";
Mech. Dev. 59:153-164(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U36488;
HSSP; P18052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:108027; Ptprv.
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CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

DEVELOPMENTAL STAGE: Detectable in the epiblast of cocytes and throughout early mouse embryo development. In adult, expression i localized in gonadal germ cells.

SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.

SIMILARITY: Contains 10 fibronectin type III domains.
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ev. 61:213-215(1996).
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CYTOPLASMIC (POTENTIAL).

FIERONECTIN TYPE-III 1.

FIERONECTIN TYPE-III 2.

FIERONECTIN TYPE-III 3.

FIERONECTIN TYPE-III 4.

FIERONECTIN TYPE-III 6.

FIERONECTIN TYPE-III 6.

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FIERONECTIN TYPE-III 8.

FIERONECTIN TYPE-III 9.

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Matches 78
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STRAIN=R-47;
              MEDLINE=99241045; PubMed=10222200;
                                                                                       Biosci.
                                                                                                  "A neopullulanase-type alpha-amylase gene from vulgaris R-47.";
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Bacteria; Firmicutes; Bacil
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NCBI_TaxID=2026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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MEDLINE-22047855; Pubmede12051850;

X MEDLINE-22047855; Pubmede12051850;

IT "Crystal structures and structural comparison of Thermoattinomyces

IT "Ulgaris R-47 alpha-amylase 1 (TVAI) at 1.6 A resolution and

IT alpha-amylase 2 (TVAII) at 2.3 A resolution.";

IJ Mol. Biol. 318:443-453(2002).

C -i- FUNCTION: Hydrolyses of 1.4-alpha-glucosidic linkages in

C of starch. Endohydrolysis of 1.4-alpha-glucosidic linkages in

C pulhulan to form panose. Cleaves also (1-6)-alpha-glucosidic

C linkages to form maltotriose.

C -i- CATALYTIC ACTIVITY: Hydrolysis of pullulan to panose (6-alpha-D-

C glucosylmaltose).

C -i- CORACTOR: Binds 1 calcium ion per subunit.
                                                                                                                                                                                              EMBL; D13178; BAA02473.1; -.
PIR; JCC1486; JCC1488.
PDB; LBVZ; 02-MAR-99.
PDB; IG1Y; 14-MAR-01.
PDB; 1JT5; 25-DEC-02.
PDB; 1JT6; 25-DEC-02.
PDB; 1JT12; 18-DEC-02.
PDB; 1JT12; 18-DEC-02.
PDB; JJT13; 18-DEC-02.
PDB; JJT13; 18-DEC-03.
                                                                                                  3D-structure.
ACT SITE 3
ACT_SITE 3
ACT_SITE 4
METĀL 1.
METĀL 1.
METĀL 1.
METĀL 1.
  METAL HELLX
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                                                                                                                                                                                    InterPro;
InterPro;
                                                                                                                                                            Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02903; alpha-amylase_N; 1.
SMART; SM00642; Aamy; 1.
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                        Carbohydrate
                                                                                                                                                                                                                                                                                                         -1- COFACTOR: Binds 1 calcium ion per subunit.
-1- SUBUNIT: Monomer.
-1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
                                                                                                                                                                                                                                                                                                                                                                                                           Sakano Y.; "Crystal structure of Thermoactinomyces vulgaris R-47 alpha-amylase II (TVAII) hydrolyzing cyclodextrins and pullulan at 2.6-A resolution."; J. Mol. Biol. 287:907-921(1999).
                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                           IPRO06589; Alp amyl cat sub.
IPRO06047; Alpha_amyl_cat.
IPRO06418; Glyco_hydro_131g.
IPRO07110; Ig-like.
  metabolism;
  148
149
169
171
171
171
14
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19
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19
                                                                                                                                                     Hydrolase; Glycosidase; Calcium-binding;
                                                                                            CALCIUM.
CALCIUM.
CALCIUM.
CALCIUM.
CALCIUM.
CALCIUM.
                                                                                                  (VIA CARBONYL OXYGEN)
                                                                                                                   (VIA
                                                                                                                   CARBONYL OXYGEN).
TURN
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TURN
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403
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RP3_AC
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253490,
01-0CT-1996 (Rel. 34, C.
01-0CT-1996 (Rel. 34, L.
15-UTL-1999 (Rel. 38, I.
15-UTL-1999 (Rel. 38, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACACA
ARP3_1
                                                                                                                                                                                                                                                                                                                                          "Sequences, structural models, and cellular localization of the article-related proteins App2 and Arp3 from Acanthamoeba."; J. Cell Biol. 131:385-397(1995).

-!- FUNCTION: Part of a complex implicated in the control of ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAND
SEQUENCE
                    Pfam; PF00022; actin; 1. SMART; SM00268; ACTIN; 1
                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=ATCC 30010 / Neff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAND
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                                                                          EMBL; U29610; AAA93068.1;
                                                                                                                                                                                                                                                              polymerization in cells (By similarity).

-!- SUBUNIT: Belongs to a complex composed of ARP2, ARP3, P41-ARC, P34-ARC, P21-ARC, P20-ARC and P16-ARC (By similarity).

-!- SIMILARITY: Belongs to the actin family. ARP3 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96017709; PubMed=7593166; Kelleher J.F., Atkinson S.J., Pollard T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Acanthamoebidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TURN
    PROSITE;
                                                      InterPro; IPR004000; Actin_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acanthamoeba castellanii (Amoeba)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 LKIMHDAI-----GFRSTLT--GKNYTMEW
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  PS01132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSVFGPT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIVGEIWHDASGWLMGDQFDSVMNYLFRESVIRFFATGEIHAERFDAELTRARMLYPEQA
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ACTINS_ACT_LIKE; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acanthamoeba.
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                                                                                                                                  (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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                                                                                                                                http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---RLAVLFQMTYLĞTPLIYYĞDE 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96;
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989
01-MAR-1989
15-MAR-2004
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                      -!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
-ipha, beta, gamma, delta, and epsilon which are responsible different reactions of DNA synthesis.
-!- SIMILARITY: Belongs to the DNA polymerase type-9 family.
                                                                                                                                                                     Pearson B.E., Nasheuer H.P., Wang T.S.;
"Human DNA polymerase alpha gene: sequences controlli
cycling and serum-stimulated cells.";
Mol. Cell. Biol. 11:2081-2095(1991).

-!- FUNCTION: Polymerase alpha in a complex with DNA
                                                                                                                                                                                                                                                                                                                                 "Human DNA polymerase alpha gene expression is dependent and its primary structure is similar
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88196090; PubMed=3359994; Wong S.W., Wahl A.F., Yuan P.-M., Arai N. Korn D., Hunkapiller M.W., Wang T.S.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
DNA polymerase alpha catalytic subunit (EC 2.7.7.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPOA_HUMAN
                                                                                                                                                                                                                                                   MEDLINE=91172197;
                                                                                                                                                                                                                                                                     SEQUENCE OF 1-8 FROM N.A.
                                                                                                                                                                                                                                                                                                   and eukaryotic replicative DNA polymerases.";
EMBO J. 7:37-47(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P09884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural protein; Cytoskeleton. SEQUENCE 427 AA; 48635 MW; A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                        replicative polymerase.
CATALYTIC ACTIVITY: N deoxynucleoside triphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303
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                                                                                                                           DNA) (N).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPYCQAKYTFCP--TGSPIPVME---GDDDIE----VFRLQAPVWEFKYGDLLGHLKIMHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLLQIFDAVI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDTEPDKWF----KTYEGIES----VGKKPYNVDVGYERFLGPEIFFNPEIFSSDFLT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIGFRSTLTGKNYT-MEWYELFQLGNCTFPHLR-----PEMDAPFWCNQGAAC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPRCRARRWWCPWAAGKNIADLDFFIGDEAYENSKVYQITMPV---RHGQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IETNYTRIFLYSGEPTYLGNETSVFGPTGNK--TLGLAIKRFYYP---FKPHLPTKEFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NVKASPEKGAE-TWF-------DSYDCSKFVLRTFNKLA-EFGAEFKN
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                                                                                                                                                                                                                                                     PubMed=2005899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -ENWTHMEQF----WEHCIFKYLRCEPEDHHFLLTEPPLNAPENREYTAEI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.6%; Score 89.5;
20.6%; Pred. No. 3.
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                                                                                                                                                                                                                     controlling
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                                                                                                                                                                                                                                                                                                                                 cell proliferation
to both prokaryotic
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                                                                                                                                                                                                                                                                                                                                 prokaryotic
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MIM; 312040;
GO; GO:00056
GO; GO:00038
                                                                                                                                                ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003889; F:alpha DNA polymerase activity; NAS.
GO; GO:000660; P:DNA replication; NAS.
InterPro; IPR006134; DNA pol B.
InterPro; IPR006134; DNA pol B dom.
InterPro; IPR006133; DNA pol B exo.
InterPro; IPR006133; DNA pol B exo.
InterPro; IPR004578; PolZ.
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Pfam; PF03104; DNA_pol_B exo; 1.
PRINTS; PR0106; DNAPOLB.
SMART; SM00486; POLBC; 1.
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EMBL; M64481; AAA52318.1; -.
PIR; S00257; DJHUAC.
         Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                         TRUD OR AF1677
                                                   Probable tRNA pseudouridine synthase) (Uracil hydrolyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA-binding; Nuclear protein.
DNA_BIND 650 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:9173; POLA.
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                                                                                                                                                                                                                                                                                                                                                                                              WCNQGAACFFEGIDDVHWKEN---GTLVQVATISGNMFNQMAKW-VKQDNETGIYYETWN
                                                                                                                                                                                                                                                                                                                                                                                                                           ESGAMEFEDGDF---
                                                                                                                                                                                                                                FDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYE----EIPLPIRNKTLS 344
                                                                                                                                                                                                                                                                                     ETNYTRIELYSGEPTYLGNETSVFGPTGNKT-LGLAIKRFYYPFKPHLPTKEFLLSLLQI
                                                                                                                                                                                                                                                                                                                                          VKASP---EKGAET-----WFDSYD---CSKFVLRTFNKLAEFGAE-----FKNI
                                                                                                                                                                                                                                                                                                                                                                    WDKES-----EPAEEVKQEADSGKGTV----SYLGSFLPDVSCWDIDQEGDSSFSVQEVQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                    QAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKRSIGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAGDDVQVESTEEEQ 242
                                                                                                                                                                                                       FKSKPVEKN----YAFEIPDVPEKSEYLEVKYSAEMPQLPQDLKGETFS
                                                                                                                                                                                                                                                                                                                  VDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLFGKVWIESAETHVSCCVMVKNI
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1245 1376 POT
1462 AA; 165860 MW;
                                                                            (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation updat
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                                                                                                                                     STANDARD;
Archaeoglobus
                                                    hydrolyase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.6%;
20.3%;
                                                                                                                                                                                                                                                             ---FLPREMKIDLNTGKETGTPISMKDVYEEFDEKIATKYKIMK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
                                                               nnnotation update)
synthase D (EC 4.2.1.70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 88.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                     411 AA.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5'-phosphate + H(2)O.
-!- SIMILARITY: Belongs to the pseudouridine synthase trub family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Could be responsible for synthesis of pseudouridine fro uracil-13 in transfer RNAs (By similarity).
-!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390.364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF_01082; -; 1.
InterPro; IPR001656; U
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ACT_SITE 81 81 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000987; AAB89568.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01142; UPF0024;
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                                                                                                                                                                                                                                                                                                                            YGVKK---
                                                                                                                                                                                                                                                                                                                                                                                                   LSDEGDFLIIRVEKKNW-----DTLNFARVLSNALGISQKRISFAGTKDKRALTVQYFSI
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEGDDDIEVFRIQAPVWEFKYGDLIGHLKIMHDAIG-----FRSTLTGKNYTMEWYEL
                                                                                                LREGKSEEEALLSLPKNLKMMFVHAYQSYIF
                                                                                                                                                                       ---LONNYEEAFWVYVAKPFEGENEEVRKIREILWETRDAKLGLRELPKYLRYERNLLQK
                                                                                                                                                                                                          FKNIETNYTRIF-LYSGEPTYLGNE----TSVFGPTGNKTLGLAIKRFYYPFKPHLPTK 290
                                                                                                                                                                                                                                               FF-RIRVYGCRDGE--IFQETRN--ELMEKGTPNFFGLQRFGSIRFITHEVGKLI--
                                                                                                                                                                                                                                                                                     MFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWF--DSYDCSKFVLRTFNKLAEFGAE
                                                                                                                                                                                                                                                                                                                                                               FQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKE-----NGTLVQVATISGN 178
                                                                                                                                 -----EFLISLLQIFDAVIVHK-QFYLF 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AA; 47715 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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20.3%; Pred. No. 4.4;
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5; Mismatches
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STANDARD;

PRT;

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Matches
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01-AUG-1992 (Rel.:
01-AUG-1992 (Rel.:
10-OCT-2003 (Rel.:
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ACT_SITE
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00455; AMP_BINDING; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00501; AMP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_01123; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- PTM: The N-terminus is blocked.
-!- PTM: Acetylated. Deacetylation by the SIR2-homolog deacetylase activates the enzyme (By similarity).
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanothrix soehngenii.";
J. Bacteriol. 171:5430-5435(1989).
-!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U1-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acylaton Company).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000873; AMP-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P08659; 1LCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jetten M.S., Stams A.J., Zehnder A. "Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION.
MEDLINE=90008777; PubMed=2571608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eggen R.I.L., Geerling A.C.M., Boshoven A.B.P., de Vos W.M.; "Cloning, sequence analysis, and functional expression of th Coenzyme A synthetase gene from Methanothrix soehngenii in Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanothrix soehngenii.
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosaetaceae; Methanosaeta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol. 173:6383-6389(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetyl-CoA
                                                     304
                                                                                                                                                                                                                                                                                     11 RASWCWALALLWLAVVPGWSRVSGIPSRRHWPVPYKRFDERPKPD-----PYCQAKYTF
                                                                                                                                                                                                                                                                                                                                                87;
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acetylation.
     QVATISGNMFNQM---
                                                -GNAVGPAQTLHW--VFDLKD-----
                                                                                           RSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV 170
                                                                                                                                            KRAGVDVSMKEGRDVWWHDLVKGQSEECEPVWVDPEHRLYILYTSGTTGKPKGIEHATG-
                                                                                                                                                                                            CPTGSPIPVMEGDD----DIEVFRLQ--APVW---EFKY----GDLLGHLKIMHDAIGF 110
                                                                                                                                                                                                                                             RAAHCGSRAII---TVDGF-----YRRGKPVPLK----PNADEAAGGAPSVEKIIVY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                 672 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / DSM 2139;
                                                                                                                                                                                                                                                                                                                                                                                                                                              638 1
75527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               546
                                                                                                                                                                                                                                                                                                                                                                    22.9%;
                                                                                                                                                                                                                                                                                                                                                                                         4.5%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zehnder A.J.;
                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                    Score 87.5;
Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
ACETYLATION (BY SIMILARITY).
-- AKWVK--QDNE-TGIYYETWNVKASPEKGAETWFDSY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                            D3CB6AC88BAEAF65
                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acetyl-coenzyme A synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                --DDVWWCTA---
                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                             118;
                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Length 672;
                                                                                                                                                                                                                                                                                                                                           Indels 129;
                                                ---DIGWVTGHSYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the acetyl
                                                                                                                                                                                                                                                                                                                                      Gaps
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P100_HSV7J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     맑
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matrix protein; Pho
SEQUENCE 755 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U43400; AAC546
PIR; T41912; T41912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicholas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human herpesvirus (type 7 / strain JI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=57278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Large structural phosphoprotein homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P52519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P100_HSV7J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCMV UL32.
  237
                                                     311
                                                                                                          177
                                                                                                                                                                280
                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                     233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 PF-WCNQGAAC----FFEGIDD---VHWKEN-GTLVQVATISGN------MFNQMAKWV 187
                                                                                                                                                                                                                                                                                                                                                                        188 KQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  504 KERFMKEYWQF----YWDVP 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252
                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
SIYSYQILSLPLTSHRVTSFFKILTEDFDVITKSLELHAL 276
                                                  LFYNFEYWFLPMK----FPFIKITYEEIPLPIRNKTLSGL 346
                                                                                                                                                             YYPFKPH--
                                                                                                        VDPWNENGYYVTNINRLLYLGNLLITLHGSWMNMEKLALNTINEKKNAILKAIENNKNFV
                                                                                                                                                                                                             FETEFKNVAKDLLKLGSFLRWGTVTHAADYVNLTTEERAEIGENLQKAKNNMLSFTIYQI
                                                                                                                                                                                                                                                                                                                                                                                                                          PFAWISDEAKCFLSRFFENISSLPVVDIRENPWILSQCIVKTGNSINNVKTLYNNLILW-
                                                                                                                                                                                                                                                                  FGAEFKNIETNYTRI--FLYSGEPTYLGN-----ETSVFG----PTGNKTLGLAIKRF 279
                                                                                                                                                                                                                                                                                                                     ----IYFHQTLCKKKPDY-EEVWQEILKVQKILKDYLEQRQMITDYSSLTSFNKVG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLSS--LRLLGSVGEPINPEAWMWYREHIGRGELQIMDTWWQTETGTFLNSPLPITPLKP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VYAPLILGMTSLMYEGAADYPDFGRWWKNIQDHKVTVLYTAPTAVRMFMKQGAE-WPDKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVIVHKQFYLFYNFEYWFLP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSCTFPLPGYDISILDEEGNEVPLGSGGNIVALKP--YP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEPTY--LGNETSVFGPTGNKT-LG-----LAIKRFYYPFKPHLPTKEFLLSLLQIF--D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC54672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5) to the EMBL/GenBank/DDBJ databases.
THE LARGE STRUCTURAL PHOSPHOPROTEINS OF HSV-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 87.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4083744CCC3F91DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                          LPTKEFLLSLLQ----IFDAVIVHKQFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PP100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                                                                                                                                                                                                                                                                                                        -LRTENKLAE 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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ESULT 10
HSD_EMENI
D CHSD_1
MEDLIAL T., Fuj...
Motoyama T., Fuj...
Gen. Genet.
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                  TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chitin synthesis.";
Fungal Genet. Biol. 20:153-167(1996).
Fungal Genet. Biol. 20:153-167(1996).
-!- FUNCTION: Plays a major role in cell wall biogenesis.
-!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1,4)-(N-acetyl-beta-D-beta-D-beta-D-lucosaminyl)}(N) = UDP + {(1,4)-(N-acetyl-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta-D-beta
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15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
16-OCT-2001 (Rel. 42, Last annotation update)
Chitin synthase D (EC 24.1.16) (Chitin-UDP acetyl-glucosaminyl transferase D) (Class-V chitin synthase D).
                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announcs/or send an email to license@isb-sib.ch).
SEQUENCE
                                                                                                                                                                             Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96406387; PubMed=8810520; Specht C.A., Liu Y., Robbins P.W., Bulawa C.E., Ias Winter K.R., Riggle P.J., Rhodes J.C., Dodge C.L., Borgia P.T.; Borgia P.T.; The chsD and chsE genes of Aspergillus nidulans ar
                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97188530; PubMed=9037115;
Motoyama T., Fujiwara M., Kojima N.,
Mol. Gen. Genet. 253:520-528(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eurotiales; Trichocomaceae; Emericella. NCBI_TaxID=162425;
                                                                 TRANSMEM
                                                                                      TRANSMEM
                                                                                                                TRANSMEM
                                                                                                                                                     Iransferase; Glycosyltransferase; Transmembrane;
                                                                                                                                                                                                                     InterPro; IPR004835; Chitin_synth_fng
InterPro; IPR001199; Cyt_B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERRATUM
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"The Aspergi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96285568; PubMed=8709948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=FGSC 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Emericella nidulans (Aspergillus nidulans)
                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glucosaminyl) (N+1).

SUBCELLULAR LOCATION: Plasma membrane-bound.

SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY. SUBFAMILY

V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yama T., Fujiwara M., Kojima N., Horiuchi H., Ohta A., Takagi M., Aspergillus nidulans genes chsA and chsD encode chitin synthases have redundant functions in conidia formation.", Gen. Genet. 251:442-450(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chsD and chsE genes of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMENI
                                                                                                                                                                             PF03142;
PF00173;
                                                                                                                                                                                                                                                                    U52362;
                                                                                                                                                                                                                                                                                         D83246;
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                     221
476
1039
1073
1073
                                                                                                                                                                                                                                                                 BAA11866.2; -.
AAA97482.1; -.
                                                                                                                                                                             Chitin_synth_2; 1. heme_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
AA;
                  241
496
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to the
133504
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ne EMBL/GenBank/DDBJ
MW;
                                       POTENTIAL.
POTENTIAL.
                     POTENTIAL.
                                                                                    POTENTIAL.
                                                                                                           POTENTIAL.
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D6157184F154EDE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iartchouk N.,
L., Culp D.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                     Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     their roles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Α.,
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RESULT 11
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Best Local Similarity
Matches 75; Conser
                                                                                                                                                                        Brenig B.;
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                     P16960;
01-AUG-1990 (Rel. 15, Created,
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Rvanodine receptor 1 (Skeletal muscle-type ryanodine
Rvanodine receptor 1 (Skeletal muscle-type ryanodine).
                                                                             "Genomic receptor
                                                                                                                                                                                                                         STRAIN=Norwegian Landrace; TISSUE=Skeletal muscle; MEDLINE=93036581; PubMed=1329581; Harbitz I., Kristensen T., Bosnes M., Kran S., Davies W.; Harbitz I., Kristensen T., Bosnes M., Kran S., Davies W.; "DNA sequence of the skeltal muscle calcium release channel cDNA and verification of the Arg615-->Cys615 mutation, associated with porcine malignant hyperthermia, in Norwegian landrace pigs."; Anim. Genet. 23:395-402(1992).
SEQUENCE OF 4785-5035 FROM N.A.
MEDLINE=91065640; PubMed=2174405;
Harbitz I., Chowdhary B., Thomsen P
Kran S., Gustavsson I., Christensen
                                                                                                       MEDLINE=94117003;
Leeb T., Schmolzl
                                                                                                                                 STRAIN=German
                                                                                                                                               SEQUENCE OF 1129-2643 FROM N.A.
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
[1]
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                              organization of the porcine (RYR1) gene coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLY--
                                                                 (RYR1) gene coding 18:349-354(1993).
                                                                                                                                                                                                    OF 1129-2801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VCGTPPTRLKINEIGSGYMIFHGQAYDLTKSTHPAAAGIPDMTNVLYDLPHKYGGQDGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYC---SVITEWAPDFVLKCFGMPQKAQRSAWREKIG-LISIILMIAAFVGFLTFGFTAT
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                                                                                                                                                                        (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                   Landrace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343
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                                                                                                                     PubMed=8288238;
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                                                                                                                                                                                                    FROM
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                                                                                                                                  TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VSLIFILSIVIVKFAFALLFQ-
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                                                                             region
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Pred. No. 20;
44; Mismatches
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                                                                                                       Brenig
 en K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LYSGEPTYLG---NETSVFGPTGNKTLG-LAIKR 278
                                                                              ne skeletal musc
4624 to 7929.";
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 Davies W.,
Hauge J.G.;
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                                                                                            muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -WFLAPRFAAQKTSMGAVDSKA
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               Kaufman
                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                            ryanodine
                                                                                                                                                                                                                                                                                                                                                                                                                               receptor)
               ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                (RyR1)
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 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dihydropyridine receptor.

-!- MISCELLANEOUS: Ryanodine is an alkaloid that binds to the Ca-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: Homotetramet (Forestata).
-!- MISCELLANEOUS: The calcium release channel is modulated by calcium ions, magnesium ions, ATP and calmodulin.
                                               DOMAIN
                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the ryanodine receptor family.
-!- SIMILARITY: Contains 5 MIR domains.
-!- SIMILARITY: Contains 3 SPRY domains.
                                DOMAIN
                                                                               DOMAIN
                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                  Phosphorylation;
                                                                                                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50919; MIR; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ions, magnesium ions, ATP and calmodulin. MISCELLANEOUS: The calcium release channel activity resides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constitutes the 'foot' structure spanning the junctional between the SR and the T-tubule. It is possible that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sarcoplasmic reticulum. Contraction of skeletal muscle triggered by release of calcium ions from SR following depolarization of T-tubules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Communication between transverse-tubules and sarcoplasmic reticulum. Contraction of skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homotetramer (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure interacts with the cytoplasmic region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-terminal region while the remaining part of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X62880; CAA44674.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                 PF00622;
                                                                                                                                                                                                                                                                                                                                                                                                                               PF01365;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PF02815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X69465; CAA49225.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X68247; CAA48318.1;
                                                                                                                                                                                                                                                                                                                                                SM00472; MIR; 4.
SM00449; SPRY; 3.
                                                                                                                                                                                                                                                                                                                                                                              PR00795; RYANODINER.
                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003032; RyR.
IPR003877; SPRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR005821; Ion trans. IPR003608; MIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002048;
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4274
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4787
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                                                                                                                                                                                                                                                                                                                                                                                              ; RYDR_ITPR; 2.
; RYR; 4.
; SPRY; 3.
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Ca/Na_pore.
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Best Local
                                                                                                                                                                                                                                                                          MOUSE
                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
3-oxo-5-alpha-steroid 4-dehydrogenase 2 (EC 1.3.99.5)
5-alpha-reductase 2) (SR type 2) (5 alpha-SR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CONFLICT
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CARBOHYD
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CARBOHYD
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                      Q99N<u>9</u>9
                                                                                                                                                                                                                                                                 S5A2 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                           type II gene by progesterone in brain."; Nucleic Acids Res. 30:1387-1393(2002).
                                                                               Takeyama K., Kato S.;
                                                                                                                                                                              Mus musculus
                                                                                                                                                                                         SRD5Ā2 OR 5ART2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                  -!- FUNCTION: Converts testosterone into
                                                                                                     MEDLINE=21882004; PubMed=11884637;
                                                                                                                 rissue=Kidney;
                                                                                                                          SEQUENCE FROM N.A.
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  and progesterone or conticosterone into 5-alpha-dihydrotestosterone and progesterone or conticosterone into their corresponding 5-alpha-3-oxosteroids. It plays a central role in sexual differentiation and androgen physiology (By similarity). CATALYTIC ACTIVITY: A 3-oxo-5-alpha-steroid + acceptor = a 3-oxo-delta(4)-steroid + redword -------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RES
 delta(4)-steroid
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PRO-RICH.
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SPRY 3.
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acceptor
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Best Local S
Matches 35
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O52972;
16-OCT-2001 (Rel. 40, Createu,
16-OCT-2001 (Rel. 40, Last sequence update,
16-OCT-2001 (Rel. 40, Last annotation update)
Antigen 85-C precursor (85C) (Antigen 85 complex C) (Ag85C) (Mantigen 85-C precursor (85C) (Fibronectin-binding protein C)
Annaferase 85C) (EC 2.3.1.-) (Fibronectin-binding protein C)
              Mycobacterium avium.";
Infect. Immun. 65:3680-3685(1997).
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=ATCC 15769;
                                                                                                                                                                               Yamada 1
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Ohara N., Ohara-Wada
                                                                                                                                                                                                                                                                                                                                  Corynebacterineae;
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Pfam; PF02544; Steroid dh; I
PROSITE; PS50244; S5A_REDUCTASE; 1.
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                                                                                                                                                                                                                                                                                                               _TaxID=1764;
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maintaining
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                                                                                                                                                                                           PubMed=9284137;
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92 F
166 F
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28619 MW;
cell
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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Best Local S
Matches 68
mutant.";
Mol. Endo
[2]
                                                                                                                                TISUUE-Manmary gland;
TISUUE-Manmary gland;
MEDLINE-99032537; PubMed-9817599;
                                                                                                                                                                                                                                                                                                                                                                  TM16 HUMAN STANDARD; PRT; 564 AA.
095361; Q72612; Q96BB8; Q96343;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tripartite motif protein 16 (Estrogen-responsive
                                                                                         "The
                                                                                                             Liu H.-L.C., Golder-Novoselsky Zajchowski D.A.;
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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ACT_SITE
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                                                                 "The novel estrogen-responsive regulated in cells expressing a
                                                                                                                                                                                                                                                                                                                           TRIM16 OR EBBP.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAMOH
                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D87323; BAA24161.1;
HSSP; P31953; 1DQY.
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-!- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND
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PF00756; Esterase; 1.
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274
306
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Pred. No. 8.8;
26; Mismatches
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                                                                 box prote estrogen
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PXCUZLHHAXA

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A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
Chenrach A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                     Pfam; PF00622; SPRY, 1. —
Pfam; PF00643; zf-B box; 1. —
PRINTS; PR01406; BBOXZNFINGER.
SMART; SM00336; BBOX; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC001564; AAH01564.1; -.
EMBL; BC015674; AAH15674.1; -.
EMBL; BC053514; AAH53514.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyms=Beta;
IsoId=095361-2; Sequence=VSP 009098;
IsoId=095361-2; Sequence=VSP 009098;
-!- TISSUE SPECIFICITY: Highest levels found in testis, ovary, smal intestine, colon, placenta, heart, skeletal muscle and mammary gland. More highly expressed in the fetus than in the corresponding adult tisues. Expressed in basal keratinocytes. corresponding adult tisues. Expressed in basal keratinocytes.-!- SIMILARITY: Belongs to the TRIM/RBCC family.
-!- SIMILARITY: Contains 1 B30.2-like domain.
                                                                                                                                                                                                                                                                                                                            GO; GO:0005737; C:cytoplasm; TAS
InterPro; IPR001870; B302.
InterPro; IPR00574; PRY.
InterPro; IPR003877; SPRY_recepto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement ( or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
                                      PROSITE; PS50119; ZF_BBOX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
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MEDLINE=22037893; PubMed=11919186;
Beer H.-D., Munding C., Dubois N., Mamie
"The estrogen-responsive B box protein:
       inc-tinger;
                                                                                                                                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lung, Placenta, and Skill;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             keratinocyte differentiation."
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IsoId=095361-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). FUNCTION: May play a role in the regulation of keratinocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF096870; AAC79080.1; -. BC001564; AAH01564.1; -.
                                                                    SM00589; PRY; 1
SM00449; SPRY; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:17241; TRIM16.
                                                                                                                                                                                                                                                                                      IPR000315; Znf_Bbox
Zinc; Repeat; Coiled coil; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277:20740-20749(2002).
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                                                                                                                                                                                                                                                                                                                            PRY. receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mamie C., Hohl D., Werner S.; tein: a novel regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2)
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    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDILINE=87319675, PubMed=3498215,
Hession C., Decker J.M., Sherblom A.P., Kumar S., Yue C.C.,
Mattaliano R.J., Tizard R., Kawashima E., Schmeissner U.,
Heletky S., Chow E.P., Burne C.A., Shaw A., Muchmore A.V.,
"Uromodulin (Tamm-Horsfall glycoprotein): a renal ligand fo
                                                                                          "Identification of human uromodulin glycoprotein.";
                                                                                                            MEDLINE=87177970; PubMed=3453112; Pennica D., Kohr W.J., Kuang W.-J., Chen E.Y., Goeddel D.V.;
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ZN_FING
ZN_FING 1:
DOMAIN 1:
lymphokines.";
                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                            01-AUG-1988 (Rel. 08, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Uromodulin precursor (Tamm-Horsfall urinary glycoprotein) (THP).
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                         GMOD.
                                                                                                                                                                                                                                                         UROM_HUMAN
P07911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                cience 236:83-88(1987).
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                                                                                                                                                                                                                                                                                                                                                             472
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                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                                                                                      440
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                                                                                                                                                                                                                                                                                                                                                                                                                                           386 LRLQEENRKVINTTPWEHPYPDLPS--RFLH----WRQVLSQQSLYLHRYYFEVEIFGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 SRVSGIPSRRHWPVPYKRFDFRPKPDP----YCQAKY--TFCPTGSPIPVMEGDDDIEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                NETGIYYETW----NVKASPEKGAETWFD--
                                                                                                                                                                                                                                                                                                                                         -FGAEFKNIETNYTRIFLYSGEP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRLQ----APVWEFKYGDLLGHLKIMHDAIGFRSTLTGKN-YTMEWY---ELFQLG
                                                                                                                                                                                                                                                                                                                                                           --NGKEFTAWYSDMETPLKAGPFRRLGVYIDFPGGILSFYGVEYDTMTLVHKFACKFSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQVSAVVQRKYW-----TSKPEPSTREQFLQYAYDITFDP
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126
165
243
320
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                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                  STANDARD;
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246
5465 F
521 K
541 N
561 V
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                                                                                                                                                                                                                                                                                                                                                                                                     -GLTC--KGIDRKGEERN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 83.5; DI
Pred. No. 16;
11; Mismatches
                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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/FTId=VAR_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform 2).
/FTId=VSP_009098.
/E-> D (in dbSNP:2074890)
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COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
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                                                                                                 Tamm-Horsfall urinary
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                                                                                                                    Aggarwal B.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 564;
                                                                                                                                                                                                                                                                                                                                                                               --SYDCSKFVLRTFNKLAE-
                                                                                                                                                                                                                                                                                                                                                                                                    --SCISGNNFSWSLQW----
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                                     .c.,
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Science

237:1479-1484(1987)

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GO; GO:0015025; F:GPI-anchored membrane-bound receptor; TAS.

GO; GO:0016968; P:cellular defense response; TAS.

GO; GO:00068285; P:negative regulation of cell proliferation; TAS.

InterPro; IPR00152; Asx hydroxyl_S.

InterPro; IPR001881; EGF Ca.

InterPro; IPR001507; EdF_like.

InterPro; IPR001507; Endoglin/CD105.
                              CARBOHYD
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                             CARBOHYD
                                                       CARBOHYD
                                                                      DISULFID
                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                        PROSITE; PS00010; ASX HYDROXYL; 2.
PROSITE; PS00122; EGF 1; FALSE NEG.
PROSITE; PS01186; EGF 2; 3.
PROSITE; PS0016; EGF 3; 3.
PROSITE; PS01187; EGF CA; 2.
PROSITE; PS00682; ZP_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0023; ZPELLUCID; SMART; SM00179; EGF_CA; 2. SMART; SM00241; ZP; 1.
                                                                                                                                                                                                                                               Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M15881; AAA36798.1; -.
EMBL; M17778; AAA36799.1; -.
PIR; A30452; A30452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rindler M.J., Naik S.S., Li N., Hoops T.C., Perald: "Uromodulin (Tamm-Horsfall glycoprotein/uromucoid) phosphatidylinositol-linked membrane protein."; J. Biol. Chem. 265:20784-20789(1990).
                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008; EGF; 3.
Pfam; PF00100; zona_pellucida; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:12559; UMOD.
MIM; 191845; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlycoSuiteDB; P07911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P07204; IADX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91065873; PubMed=2249987; Rindler M.J., Naik S.S., Li N., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        urine.
TISSUE SPECIFICITY: Synthesized by the kidneys and is the most abundant protein in normal human urine.
SIMILARITY: Contains 3 EGF-like domains.
SIMILARITY: Contains 1 ZP domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Attached to the membrase then cleaved to produce a soluble form which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 265:20784-20789(1990).

FUNCTION: NOT KNOWN. MAY PLAY A ROLE IN REGULATING THE CIRCULATING ACTIVITY OF CYTOKINES AS IT BINDS TO IL-1, IL-2 AND THE WITH HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFFINITY.
      ignal
                                                                                                                                                                                                                                                                                                                                                                            ZPELLUCIDA.
      Membrane; GPI-anchor;
Hoops T.C., Peraldi M.-N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane by
m which is se
                                                                                                                                                                                                                                                             EGF-like domain
                                         (POTENTIAL)
                             (POTENTIAL)
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                                                                                                                                                                                              (POTENTIAL)
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                                                                                                                                                                                                                                   Matches
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Best Local
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CARBOHYD
CONFLICT
SEQUENCE
                                            252
                                                                  164
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                                                                                                                                       152
                                                                                                                                                                                     118
                                                                                                                                                              67
                                                                                                                                                                                                         13 SWCWALALL-----WLAVVPGWSRVSGIPSRRHWPVPYKRFDFRPKPDPYCQAKYTFCP
                                                                                                                                                                                                                                 53;
                                                                                                                                                                                                                                             Similarity
                                                                                        GYACDTDLRGWYRFVGQGGARMAETCVPVLRCNTAAPMWLNGTHPSSDEGIVSRKACAHW
                                                                                                                                                         TGSPIP----VMEGD-----DDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGK 117
                                            SGHCCLWDASVQVKACAGG--
                                                                   KENGTL---
                                                                                                                                       PGSCGPGLDCVPEGDALVCADPCQAHRTLDEYW-
                                                                                                                                                                                   SHCHALATCVNVVGSYLCVCPAGYRGDG--
                                                                                                                                                                                                                                                                               640 AA;
                                                                                                                                                                                                                                                                                          322
396
565
                                                                                                                                                                                                                                 Conservative
         8
                                                                 VQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPE
                                                                                                              -WYELFQLGNCTF----PHLRPEMDAPFWCNQGAACFFEGIDD----VHW 163
                                                                                                                                                                                                                                                                           /FTId=CAR_000178. (PG 322 N-LINKED [GLCNAC. . .) (PG 396 N-LINKED (GLCNAC. . .). 565 H -> D (IN REF. 2). 69760 MW; D26A07A76353AE48 CRC64;
                                                                                                                                                                                                                                          4.3%;
        2004, 14:04:36
                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                            Score 83.5;
Pred. No. 1
                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                             19;
                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                68;
                                            YYVYNLTAPPE
                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                   -----HCE-----CS
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1 protein - protein search, using sw model
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SPTREMBL_25:*

1: sp_archea:*
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9: sp_phage:*
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11: sp_virus:*
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1927
1 MRRGAGAARGRASWCWALAL.....IKITYBEIPLPIRNKTLSGL 346
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

025330 helicobacte	.6 025330	38 1	12	4.9	94	16
Q9tym2 caenorhabdi	Q9TYM2			4.9	94	15
Q9vpl9 drosophila	Q9VPL9			5.0	95.5	14
Q13785 homo sapien	Q13785			5.0	95.5	13
Q9zv89 arabidopsis				5.0	95.5	12
Q8ids4 plasmodium	5 QBIDS4	508 5		ъ. О	96	11
Q9erk5 mus musculu	.1 Q9ERK5			5.0	96.5	10
QBiau5 plasmodium	Q0IAUS			5.1	97.5	9
Q8nbj6 homo sapien	Q8NBJ6			5.1	98	00
Q8a3v2 bacteroides	.6 Q8A3V2			5.2	99.5	7
Q8nih1 trichophyto	Q8NIH1			5.2	101	0
O17575 caenorhabdi				5.3	101.5	, UT
Q86jg6 dictyosteli	_			10.5	202	1,42
Q86157 dictyosteli				12.2	235	ند)
Q8c054 mus musculu				74.2	1429	2
Q8r152 mus musculu	L1 Q8R152	36		75.3	1451	ىر
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4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7		4.8	4.8	4.8	4.9
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Q8mmw0 dictyosteli	Q91nq2 taura syndr	029397 bos taurus	_	Q7z9m6 trichoderma	5	09yc61 aeropyrum p	Q9aip9 methylococc	0				Q8mln6 drosophila		CO	ω			azoa			Q9bvz9 homo sapien		001702 caenorhabdi			Q8mqi2 drosophila	l escheric	Q8whw9 psilotum nu

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190 DNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFL 249	120 GNCTFPHLRPDKSAPFWCNQGAACFFEGIDDKHWKENGTLSVVATISGNTFNKVAEWVKQ 179		60 PIPVMKDNDVIEVLRLQAPIWEFKYGDLLGHFKLWHDAVGFRSTLTGKNYTIEWYELFQL 119	HE TO	4 AHWRPALALALGLATILGASPTSGQRWPVPYKRFSFRPKTDPYCQAKYTFCPTGS 59	12 ASWCWALALLMLAVVPGWSRVSGIPSRRHWPVPYKRFDFRFKPDPYCQAKYTFCPTGS 69	Query Match 75.3%; Score 1451; DB 11; Length 336; Best Local Similarity 76.6%; Pred. No. 1.6e-118; Matches 258; Conservative 31; Mismatches 42; Indels 6; Gaps 2;	SEQUENCE 336 AA; 38911 MW; D50D74C45483BE1B CRC64;	P		25487; AAH25487.1;	Submitted (MAR-2002) to the EMBT/GenBank/DDB/I databases	SECULANCE FROM N.A.		3I_TaxID=10090;		tazoa; Chordata;	Mus musculus (Mouse).	1	Similar to cercoid-linofuscinosis neuronal s (Frament)	(market 21, hast	(TrEMBLrel. 21, Created)		Q8R152 PRELIMINARY; PRT; 336 AA.	152	OLT 1

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Nature 420:563-573(2002).
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MGD; MGI:2442253; Cln5.
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Q8C054;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
51milar to CEROID-LIPOFUSCINOSIS neuronal protein 5
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                                                                                           Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ
EMBL; AC116982; AAO51609.1; -.
Hypothetical protein.
SEQUENCE 378 AA; 42306 MW; 2CF33D60851FD03
                                                                                                                                                                                                                                                                                        MEDLINE-2209262; PubMed-12097910; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.. "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Last seque 01-JUN-2003 (TrEMBLrel. 24, Last annot Hypothetical protein. Dictyostelium discoldeum (Slime mold) Eukaryota; Mycetozoa; Dictyosteliida;
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(TrEMBLrel. 24,
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Score 202; DB
Pred. No. 2.7e
53; Mismatches
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                            2.7e-09;
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                                                   DB 5;
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                                                Length 378;
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Matches

Conservative

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130;

Indels

30;

Gaps

8

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PIR; T18995; 1100000:

WormPep; C06B8.7; CE30854.

GO; GO:0016020; C:membrane; IEA.

GO; GO:00016020; F:endopeptidase inhibitor activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

InterPro; IPR002160; Kunitz_legume.

InterPro; IPR001190; Srcr_receptor.

Pfam; PF00530; SRCR; 3.

Pfam; SM00202; SR; 3.

SMART; SM00202; SR; 3.
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Best Local Similarity
Matches 103; Conserv
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PROSITE; PS50287; SRCR_2; 3.
SEQUENCE 3118 AA; 355828 MW; FF2
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01-JAN-1998 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for investigating biology.";
Science 282:2012-2018(1998).
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MEDLINE=99069613; PubMed=9851916;
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                                    NCSVTDNSGPIIESHRDLYASANVFHW--ILWSNTFANNSRSGIAVALPDTYDLLAKQTH 1559
                                                                                                                     GRISNRWNNEKIWLOKV-NFTRNSEAVMWIHSPOHAVVP------GTPIAEITYHFD 1500
                                                                                                                                                            GRASWCWALALLWLAVVPGWSR----VSGIPSRRHWPVPYKRFDFRPKPDPYCQAKYTF-
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                                                                               -CP-TGSPIPVMEGDDDI----EVFRLQAPVWEFKYG-
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                                                                                                                                                                                                         Conservative
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-GHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFP-----HLRPE 140
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22, Last sequence update)
25, Last annotation update)
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Caenorhabditis.
                                                                                                                                                                                                     52;
                                                                                                                                                                                                                          Score 101.5;
Pred. No. 27;
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                                                                                                                                                                                                       143;
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                                                                                                                                                                                                     165;
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                                                                               98
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Trichophyton rubrum encoding metalloprotease.";
RI Submitted (AUG-2001) to the EMBL/GenBank/DDBJ data
DR EMBL; AF407189; AAN03640.1; -.
DR GO; GO:0005776; C:extracellular; IEA.
GO; GO:0004222; F:metalloendopeptidase activity; I
DR GO; GO:0004270; F:zinc ion binding; IEA.
DR GO; GO:0008770; F:zinc ion binding; IEA.
DR GO; GO:000870; P:proteolysis and peptidolysis; IEB.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEB.
DR GO; GO:0008570; F:metalloendopeptidase M36.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEB.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEB.
DR GO; GO:000501842; Peptidase M36.
R InterPro; IFR006025; Pept M Zn BS.
R Pfam; PF02128; Peptidase M36; I.
R PROSTIE; PS00142; ZINC_PROTEASE; 1.
M Metalloprotease; Protease.
W Metalloprotease; Protease.
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Best Local S
Matches 61
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01-OCT-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Onygenales; Arthrodermataceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichophyton.
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237
                                                                                                                         141 RAPV---EKRDFSGPMRAFHGACKALNLPINADKATI----QTMNEHEVMFVGT-----
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                                                                                                                                                      86
                                                                                                                                                                                   61;
                                                                                                                                                                                   Similarity 22.8
51; Conservative
NVVDYVSHATYQVYRWPIPDPTEGKREIVENPWNLKTSP----FTWISDGKTNYTTTRGN
                                                                                      RPEMDAPFWCNQGAACFFEGIDDVHWKENGTLV---QVATISGNMF---
                                                                                                                                                      QAPVWEFKYGDILGHLKIMHDAI------GFRSTLTGKNYTMEWYELFQLGNCTFPHL
                                                            SGAMSDP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFYLFYNF----EYWFLPMKFPFIKIT----YE-EIPLPIRNK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLHGRVYEDKNITLITERWYSFPYNYRPFRPYRITRDVTIMPGATLYIEQNVEVHVWPNV 1837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RIFLYSG-----EPTYLGNETSV-----FGPTGN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEKNLICERNRFFFNWG----HWMIKLDATSQYLRQIDVPSYVQYNYIEK-NRFINQRGD 1662
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                           -NOMAKWVKODNETG---IYYETWNVKASPEKGAETWFDSYDCSKFVLRTF
                                                            -QGKLCYMA---
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Last annotation update)
cotease 3.
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Pred. No. 3.6;
34; Mismatches
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                                                            KEDGTLALTWRVETDMGDNWLLSYVDAKETDKVH
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                                                            236
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Best Local S
Matches 52
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Q8A3V2;
                                                               Q8NBJ6; PRELIMINARY; PRT; 682 AA.
Q8NBJ6; (7EMBLrel. 22, Created)
01-OCT-2002 (TEMBLrel. 22, Last sequence update)
01-OCT-2002 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
Hypothetical protein NT2RP2002760.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat Mammalia; Eutheria; Primates; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-VPI-5482 / ATCC 29148;
MEDLINE-22550858; PubMed-12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron
Science 299:2074-2076(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE016937; AA077958.1; -.
GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl
GO; GO:009975; P:carbohydrate metabolism; IEA.
InterPro; IPR006710; Glyco_hydro_43.
Pf4am; PF04616; Glyco_hydro_43; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Bacteroidetes; Bac
Bacteroidaceae; Bacteroides
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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Complete proteome.
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  SEQUENCE
                                              NCBI_TaxID=9606;
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InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005889; SV2.
InterPro; IPR005988; SV2.
Pfam; PF00083; sugar tr; 1.
TIGRPAMS; TIGR01299; Synapt SV2; 1.
PROSITE; PS008217; SUGAR_TRANSPORT 2; 1.
PROSITE; PS00217; SUGAR_TRANSPORT 2; 1.
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Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura
Nagahari K., Sugano S., Isogai T.,
"HRI human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                         Seeger K., Murphy L., Harris D., Berriman M., Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ EMBL, ALB4507; CAD51265.1; --
GO; GO:0007049; P:cell cycle; IEA.
InterPro; IPR001373; Cullin.
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01-JUN-2003 (TrEMBLrel. 24, La
Cullin-like protein, putative.
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                                                                                                     Pfam; PF00888; Cullin; 1.
SMART; SM00182; CULLIN; 1.
PROSTIE; PS50069; CULLIN 2; 1.
SEQUENCE 804 AA; 97162 MW;
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Eukaryota; Alveolata; Apicomplexa;
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682 AA; 76660 MW.
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                                 Length 804;
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9ERK5
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Best Local S
Matches 78
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InterPro; IPR003967; FN_III-like.
InterPro; IPR000397; TNT_phosphatase.
InterPro; IPR000347; TyT_pp.
Pfam; PF00102; Y_phosphatase; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00104; PTS; 1.
SMART; SM00194; PTS; 1.
SMART; SM00194; PTS; 1.
PROSITE; PS00183; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00185; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_7TP; 2.
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Q9ERK5;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural characterization and chromosomal localization of the cDNA and gene encoding the bone tyrosine phosphatase, mOST-PTP."; Gene 257:195-208(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-MAR-2001 (TrEMBLrel. 16, Created)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Osteotesticular protein tyrosine phosphatase (EC 3.1.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF300701; AAG28768.1;
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                                                                                                                                                                      Hydrolase.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:108027; Ptprv.
G0:0016787; F:hydrolase activity; IEA.
G0:0004727; F:prenylated protein tyros
G0:0006470; P:protein amino acid depho
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                32
                                                                                                               Similarity
                RQGGGPPLSVNVSSRGKPT---SLFLSWVAAEPGGFDYALCLRAMNLSGFPEGQQLQAHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLRYLDRYY--VEYNSSLCLSAYTKNIFKI-----TLFNELR-----
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                                                                                                                                                                    MW;
                                                                                                             Score 96.5;
Pred. No. 33;
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                                                                                          Indels
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RESULT
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Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harris B., Lennard N., Clark L., Line A., Barron A., Corton Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., D Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. EMBL, AL84499; CAD52545.1; -.
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01-MAR-2003 (TrEMBLrel.
Hypothetical protein.
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Eukaryota; Alveolata;
NCBI_TaxID=36329;
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SEQUENCE 508 AA; 58842 MW;
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                                                                                                                                                                          GLAI----
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                                                                                                                                                                                                                                                                                                                                     AETWFDSYDCSKFVLRTFN-----
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                                                           YMLNYINEKKLDIFKKITLS
                                                                                            IKITY-EEIPLPIRNK-TLS 344
                                                                                                                                 GRIKPFNVLGACQLPSLCTPSYTTSNNNNNNNNNNNNNNNNNNNNNNNNNNNLFGPFENKTL
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Pred. No. 7.4;
                                                           371
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Best Local S
Matches 53
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Q9ZV89;
01-MAY-1999
01-MAY-1999
                                                                                                                                                                                Q13785;
01-NOV-1996
01-NOV-1996
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Li J., Liu S., Kremenetskaia I., Luros J., Araujo R., Buehler E., Conway A.B., Dewaar K., Feng J., Kim C., Li Y., Shinn P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A., Federspiel N.A., Theologis A., "Arabidopsis thaliana chromosome 1 BAC F9K20 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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InterPro; IPR004253; DUF231.
Pfam; PF03005; DUF231; 1.
                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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    SEQUENCE
                                                                                                                Homo sapiens
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                                        NCBI_TaxID=9606;
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  FROM N.A
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                                                                  Chordata;
Primates;
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Last annotation updat
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Pred. No. 5
                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                           PRT;
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RESULT 14
Q9VPL9
ID Q9VPL
ID Q9VPL
AC Q9VPL
AC Q9VPL
DT 01-00
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9VPL9; Q9N164;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CG3696 protein (KISMET-L long isoform).
KIS OR CG3660 OR CG3696 OR CG18326.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Roptera, Endopterygota; Diptera, Brachycera; Muscomorpha;
Rephydroidea; Drosophilidae; Drosophila.
MEDLINE-2019606; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M12413; AANUL
- n07850; LPHUB.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006610; P:transport; IEA.
InterPro; IPR000531; TonB boxC.
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Wei C.F., Chen S.H., Yang C.Y., Marcel Y.L., Milne R.W.
Sparrow J.T., Gotto A.M. Jr., Chan L.;
"Molecular cloning and expression of partial cDNAs and
"Molecular cloning and expression of partial cDNAs and
acid sequence of a carboxyl-terminal fragment of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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NON TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OFPGKFGIYTREELCTMF-IREVGTVLSQVYSKVHNGSEILFSYFQDLVITLPFELRK 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YYPFKPHLPTKEFLLSLLQIFDAVIVHKQFY-----LFYNFEYWFLPMKFPFIK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWKDKAQNLYQELLTQEGQASFQGLKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFKNIETN-YTRIFLYSGEPTYLGNETSVEGPTGNKTLGLAIK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRRNLQDHAEWVYQ----GAIREIDDIDERFQKGASGTTGTYQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQIKVNWEEEAASGLLT--SLKDNVP-----KATGVLYDYVNKYHWEHTGLTLREVSSK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG-TLVQVATI 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSAPSPAVGTVGMDMDEDDDFS-----KWNFYYSPQSSPDKKLTIFKTELRVRESDEE
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ilarity 20.5%;
Conservative 3
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Pred. No. 16;
9; Mismatches 125;
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de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A. Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
A. Nelson D.R., Nelson K.A., Ni J., Muzny D.M., Nelson D.L.,
A. Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A. Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A. Syirs B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A. Syirskas R., Tector C., Turner R., Vener E., Wang A.H., Wang X.,
A. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A. King S., H., Zhong F.N., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
The genome sequence of Drosophila melanogaster.";

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Vicence 287:2185-2195(2000).
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A Banzon J., An H., Balawin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
A Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
A IDegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
A Phouanenavong S., Pittman G.S., Patel S., Pfeiffer B.,
A Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
A Pholamenavong S., Sittman G.S., Puri V., Richards S., Scheeler F.,
A Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
T "Sequencing of Drosophila melanogaster genome.",
I Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Adams M.D., Celniker S
Submitted (MAR-2000) t
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                             Submitted (DEC-1999) to the EMBL; AE003590; AAF51527.3; EMBL; AF215703; AAF43004.1; HSSP; P23197; 1AP0.
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                                                                                                                                                                                                                                      errien M., Morrison D.K., Wong
Genetic Screen for Modifiers
                                                                                                                                                                                                               Drosophila.";
3ase; FBgn0001309; kis.
GO:0000785; C:chromatin; IEA
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3., Crosby M.A., M
Huang Y., F
                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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S.E., Adams M.
                                                                                                                                                                                                                                                                                                                                                                                                       (SEP-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.E., Gibbs R.A., Rubin G.M., Vente to the EMBL/GenBank/DDBJ databases.
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of a KSR-Dependent Rough
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Smith H.O.,
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InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helic:
InterPro; IPR001300; SNF2]
Pfam; PF00385; Chromo; 1.
Pfam; PF00271; helicase C;
Pfam; PF00176; SNF2 N; 1.
SMART; SM00298; CHROMO; 2.
SMART; SM00487; DEXDC; 1.
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01-MAY-2000
01-MAY-2000
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulso Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownke
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ATP-binding; Helicase; Hydrolase.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
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Y25C1A.7 OR Y25C1A.7A.
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SM00490; HELICC; 1.
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4; F:ATP binding; IEA.
6; F:ATP dependent helicase act
12; F:chromatin binding; IEA.
12; F:chromatin binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Peloderinae;
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          McMurray A., Mortimore B., O'Callaghan M.,
lfken L., Roopra A., Saunders D., Shownkeer
                                                                                                                                                                                                                                                                                                                                                                                                                              cda; Chromadorea;
Caenorhabditis.
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Waterston R.;
Submitted (PEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125459; AAD12838.1; -.
PIR; T33904; T33904.
WormPep; Y25C1A.7a; CE21474.
InterPro; IPR006977; DUF649.
Pfam; PF04893; Yip1; 1.
SEQUENCE 362 AA; 40613 MW; 42DB45A7F72F3B89 CRC64;
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STRAIN-Bristol N2;
Kalicki J., Smith A., Gibson A.;
Kalicki J., Smith C. elegans cosmid Y25ClA.";
"The sequence of C. elegans cosmid Y25ClA.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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3: geneseqp2001s:*

4: geneseqp2001s:*

5: geneseqp2003as:*

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8: geneseqp2003bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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WPI; 1999-562050/47. N-PSDB; AAZ24826.	Ruben SM, Ni J, Rosen CA, Yu G, Young PE, Feng P, Soppet DR; Wei Y, Endress GA, Duan RD, Kyaw H, Ebner R, Lafleur DW, Olsen HS; Shi Y, Moore PA;	(HUMA-) HUMAN GENOME SCI INC.	01-APR-1998; 98US-0080314P.	٠.						٠.	٠.	19-MAR-1998; 98US-0078573P.	19-MAR-1998; 98US-0078566P.	19-MAR-1998; 98US-0078563P.		18-MAR-1999; 99WO-US005804.		23-SEP-1999	WO9947540-A1.		Homo sapiens.		endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.	osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;	cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;	inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;	immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;	developmental abnormality; foetal deficiency; blood; allergy; renal;	diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;	Human; secreted protein; fusion protein; gene therapy; protein therapy;		Human secreted protein encoded by gene 16 clone HMZAD77.	ייבים איידאר פוורואי		AAY41323;		AA141323 ID AAY41323 standard; protein; 347 AA.	RESULT 1

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WESULT 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
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2000JP-00183765.
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cal disorders,
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K, Kojima
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The invention relates to primers for synthesising full length cDNA clones, 830 cDNA molecules encoding a human protain have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are used

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product

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Claim

SEQ ID NO

3978;

1380pp +

Sequence Listing; English.

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Matches 28
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                   This invention describes the isolation of a novel human secreted protein, zsig46 encoded by a gene on chromosome 13 which is mainly expressed in the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zsig46, which may be associated with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschsprung's disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger syndrome). Antibodies and other binding proteins, are used as immunoassay reagents to detect zsig46 or cells expression it, e.g. for assessing through the control of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radiostopes etc. for he weed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; zsig46; human; chromosome 13; thyroid; disease hypothyroidism; Graves; disease; thyrotoxicosis; thyroid cancer; Hirschsprung; s disease; neuronal ceroid-lipofucinosis; Wilson di Reiger syndrome; immunoassay; detection; anti-idiotypic antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins - used for diagnosis and true
diseases involving genes on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New secreted polypeptide, zsig46, and its fragments, proteins - used for diagnosis and treatment of thyro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 90-91; 101pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Pred. No. 3.2e-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ragments, related fusion of thyroid disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorder; metabolic disorder; cancer; rheumatoid arthritinhyroid disorder; neurodegenerative disorder; cardiovascular disorder; thyroid disorder; neurodegenerative disorder; cardiovascular disorder; renal failure; autoimmune disorder; hyperproliferative disorder; HIV; human immunodeficiency virus; viral infection; neuroprotective; immunostimulant; neuroleptic; nootropic; tranquiliser; antidepressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 346 AA;
Sequences AAU29380-AAU29509 represent human G protein-coupled receptor (GPCR) polypeptides of the invention. The proteins and the DNA sequence encoding them can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity By screening a human subject for the presence of mutations in GPCR DNA, GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental
                                                                                                                                                                      Nucleic acid encoding G-protein coupled receptors, useful prevention, diagnosis and treatment of mental disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                29-MAR-2000;
29-MAR-2000;
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16-MAR-2000;
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                                                                                                                                      Claim
                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                             (PHAA)
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2000US-0189961P.
2000US-0189960P.
2000US-0192155P.
2000US-019234P.
2000US-0192830P.
2000US-0192830P.
2000US-0192933P.
2000US-0192933P.
2000US-0192935P.
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2000US-0189907P.
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                                                                                                                                      274pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.5%;
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Pred. No. 2.9e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPCR; mental disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 346;
                                                      modulate GPCR activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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oid arthritis;
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                                                                                      DNA sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders such as schizophrenia, neurological disorders such as manic depression, metabolic disorders such as obesity, cancer, rheumatoid arthritis, thyroid disorders such as myxoedema, neurodegenerative disorders such as Barkinson's disease, cardiovascular disorders such as atherosclerosis, remal failure, autoimmune disorders, hyperproliferative disorders such as psoriasis and viral infections such as those caused by
                                                                             WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                     16-MAR-2000;
16-MAR-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                 G protein coupled receptor; nGPCR-x; immune response; thyroid disorder; mental disorder; thyreotoxicosis; myxoedema; inflammatory condition; Crohn's disease; cell differentiation; homeostasis; rheumatoid arthritis; renal failure; autoimmune disorder; movement disorder; CNS disorder; viral infection; human immunodeficiency virus; HIV; metabolic disorder; cardiovascular disorder; diabetes; obesity; anorexia; cardiomyopathy; porliterative disease; cancer; psoriasis; lung cancer; hormonal disorder;
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                                                        New isolated
                                                                                                                                                                          29-MAR-2000;
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29-MAR-2000;
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                                            producing
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)B; ABK81635.
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                                             the
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2000US-018991PP.
2000US-018991PP.
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2000US-019215P.
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2000US-0192830P.
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2000US-0192933P.
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                                                        nucleic
                                                                                                                                                                                                                                                                                                                                2001US-00811284.
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                                                                                                                                                                                                                                                                                                         2000US-0189783P
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2000US-0192945P
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                                             receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.3%;
                                             acid encoding a G
or which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor (nGCPR-x) #39
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Pred. No. 1.
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                                             protein coupled receptor an immune response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .8;
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                                               for mammal.
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The invention

describes

an isolated

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comprising

Claim 27; Page 44; 216pp; English.

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(C (I) is used to produce a recombinant nGPRC-x polypeptide. A polypeptide c encoded by (I) is used to induce an immune response in a mammal. nGPRC-x is used to identify a compound that binds to it and/or modulates it's c activity. (I) is used to identify animal homologues of nGPCR-x. (I) can it is used to diagnose a human subject as having a brain or genetic c predisposition disorder, such a mental disorder. (I) is used to screen it is nGPCR-x related disorder including thyroid disorders (e.g. c thyreotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g. incomposition), diseases related to cell differentiation and incomposition and concers, (NS disorders, viral infections (e.g. Human immunodeficiency virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, c anorexia, cardiomyopathies), porliferative diseases and cancers (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antiiungal; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel protein #33.
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                                                                                                                     Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.
                                                                                                                                                                                                                                           WPI; 2001-451939/48
N-PSDB; AAS22467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000; 2000US-00491404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regeneration;
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                                                                                                                                                                                                                                                                                                                                                                     Liu C,
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Pred. No. 1.8;
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Example 4; Page 543-544; 894pp; English

Claim 11; Page 359-360; 389pp; English

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ABU60973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC their active domains. The polypucides, polynucleotides and antibodies craised against the polypeptides, polynucleotides and antibodies command and prevention of disorders caused by the aberrant protein command and prevention of disorders caused by the aberrant protein command and prevention of disorders caused by the aberrant protein command and prevention of disorders caused by the aberrant protein commands which bind to the polypeptides care used to identify compounds which bind to the polypeptides complete sequencing, for chromosome or gene mapping, in the production of compounds and in generating anti-sense DNA or RNA and in generating proteins, and in generating anti-sense DNA or RNA and in generating anti-sense plan or response to a commour, in assays to determine biological activity, to raise complete sequencing to the invention may also be used to target drugs to a complete sequent and/or nerve tissue, wound healing, treating platelet contraceptive, treating osteoporosis and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, contraceptive, treating osteoporosis and osteoarthritis, anaemia, promoting contraceptive, treating osteoporosis and osteoarthritis, anaemia, promoting tringal infection or from autoimmunity, cancer, allergy, asthma, graftcontraces, personse, carema, haemophilia, thrombosis, anti-inflammatory contents of the invention of the invention. The present sequence contraces a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                          Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU60973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU60973 standard; protein; 188 AA
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                                              New isolated human nucleic acid molecule and polypeptide, identifying, diagnosing, monitoring, staging, imaging and cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Lung specific protein (LSP) #76.
                                                                                                                                                                                                              22-NOV-2000; 2000US-0252500P
                                                                                                                                                                                                                                              21-NOV-2001; 2001WO-US043612.
                                                                                                                                                                                                                                                                               06-SEP-2002.
                                                                                                                                                                                                                                                                                                            WO200268633-A2
                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                               WPI; 2002-713376/77.
                                                                                                                                              Macina RA,
                                                                                                                                                                             (DIAD-) DIADEXUS INC
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                                                                                  useful for
                                                                  treating
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                                                                  lung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated human nucleic acid (I) encoding any of 120 10-153 residue amino acid sequences (S1), given in the specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosting, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This is the amino acid sequence of a lung specific nucleic acid
                                                                                                              or veterinary medicine, particularly where avilamycins. The present aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces sequence is that of an avilamycin A biosynthetic gene cluster (ABZ37515-
                                                                                                                                                                    The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in hum or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present
                                                                            Sequence 19938
                                                                                                                                                                                                                                                                                                                               New avilamycin derivatives, useful for treatment of infections, nucleic acid encoding avilamycin synthesis enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Avilamycin; antibacterial; virucide; protozoacide; fungicide; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces viridochromogenes Avi gene cluster polypeptide frame 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP76682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 188 AA;
                                                                                                                                                                                                                                                                                         Example 1; Page 68-301; 319pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COMB-) COMBINATURE BIOPHARM AG
Local Similarity
hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             2003-018650/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGGAGAGSWVWMGGWGGGAGALWVAVVGG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus; biosynthetic gene cluster; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muehlenweg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                            AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.7%;
38.7%;
                    37.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
  Score 57.5; DB 6;
Pred. No. 5.3e+02;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB:
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trefzer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bechthold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                      Length 19938;
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    Indels
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    Gaps
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RESULT 10
ABU65190
ID ABU65
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XAX
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                                                                                                                                                                     Query Match
Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and protective antigens for new drugs and vaccine compositions to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. tuberculosis and M. leprae marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis. Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mycobacterial disease; tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABU05547 standard; protein; 214
            ABU65190;
                                         ABU65190 standard;
                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                           and prevent mycobacterial diseases, particularly tuberculosis and
leprosy. The present sequence represents a marker protein from
Mycobacterium tuberculosis and Mycobacterium leprae identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 376-377; 874pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-759885/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterioses; survival; virulence; protective antigen; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU05547;
                                                                                                                                                                                                                                                                method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2905
                                                                                                                175
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                                                                                                                                                                        10;
                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRGA---GAARGRASWCWALALLWLAVVP
                                                                                                                 RTSAIARGIYQWRWSIATLWFITV 198
                                                                                                                                          RGAGAARGRASWCWALALLWLAVV 26
                                                                                                                                                                                                                                   214 AA;
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001US-0270123P
                                         protein; 403
                                                                                                                                                                                      36.4%;
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                                                                                                                                                                                      Score 56; I
Pred. No. 8.
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                                           A
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                                                                                                                                                                                                      DB
                                                                                                                                                                                                      <u>ن</u>
                                                                                                                                                                            11;
                                                                                                                                                                                                    Length 214;
                                                                                                                                                                            Indels
                                                                                                                                                                            0;
                                                                                                                                                                            Gaps
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Human NOV105a protein.

20-MAY-2003

(first

entry)

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08-MAR-2001;
08-MAR-2001;
08-MAR-2001;
08-MAR-2001;
09-MAR-2001;
12-MAR-2001;
13-MAR-2001;
13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
14-MAR-2001;
15-MAR-2001;
                                                                                                                                                                                                                                                               20-MAR-2001

20-MAR-2001

20-MAR-2001

21-MAR-2001

22-MAR-2001

25-MAR-2001

26-MAR-2001

27-MAR-2001

27-MAR-2001

27-MAR-2001

30-MAR-2001

30-MAR-2001

30-MAR-2001

02-APR-2001

02-APR-2001

02-APR-2001

02-APR-2001

03-MAY-2001

13-MAY-2001

15-MAY-2001

15-MAY-2001

15-MAY-2001

16-MAY-2001

16-MAY-2001

31-MAY-2001

                                                   10-JUL-2001
31-JUL-2001
16-AUG-2001
10-SEP-2001
11-SEP-2001
27-SEP-2001
27-SEP-2001
11-CCT-2001
31-CCT-2001
14-NOV-2001
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                                                                                                                                                                                                                     19.
                                                                                                                                                                                                                                     18-JUN-2001;
19-JUN-2001;
                                                                                                                                                                                                                     -JUN-2001;
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2001US-0275578P
2001US-0275579P
2001US-0275601P
2001US-0275601P
2001US-0276706P
2001US-0276794P
                  2001US-0294899P
2001US-029907P
2001US-029907P
2001US-0299310P
2001US-0304354P
2001US-0312903P
2001US-0312903P
2001US-0312903P
2001US-0312903P
2001US-0312903P
2001US-0312903P
2001US-0325430P
2001US-0330360P
2001US-03303172P
2001US-0332272P
2001US-0332272P
2001US-0332272P
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2001US-0287424P.
2001US-0288066P.
2001US-0288342P.
2001US-0288528P.
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2001US-0280822P.
2001US-0280900P.
2001US-0281194P.
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2001US-0278894P.
2001US-0278999P.
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2001US-0294485P.
2001US-0294889P.
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2001US-0279995P.
2001US-0280233P.
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2001US-0279344P
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2001US-0277833P.
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2001US-0277321P.
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                                                                                                                                                                                                                                                                                                                                                   2001US-0291190P.
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片
                                                                                                                                                        Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HTV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiucer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                         Human nervous
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Query Match
Best Local :
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03-DEC-2001;
03-DEC-2001;
04-DEC-2001;
04-DEC-2002;
03-JAN-2002;
07-MAR-2002;
                                                                                              activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVX antibodies are useful for preventing or treating a disorder associated with aberrant NOVX expression or activity e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial asthma. The products of the invention can be used for gene therapy or in a vaccine. ABU65211-ABU65218 represent the NOVX polypeptides encoded by
                                                                                                                                                                                                                                                                                                                                                                                                   Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Zerhusen BD, Gusev V, Ji W, Gorman L, Miller C Patturajan M, Gangolli E, Vernet CAM, Guo X, T Fernandes ER, Casman SJ, Malyankar UM, Gerlach Spaderna SK, Catterton E, Burgess C, Leite M,
                                                                                                                                                                                                           This
                                                         Sequence 403 AA;
                                                                                     a vaccine. ABU650
ABX97008-ABX97185
                                                                                                                                                                                             cytostatic,
                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                    asthma.
                                                                                                                                                                                                                                                                                  cancer,
                                                                                                                                                                                                                                                                                                NOVX polypeptides and a disorder associated
                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-723332/78.
                                                                                                                                                                                                                                                                                                                                                                                       Lepley DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                          invention describes novel human NOVX polypeptides which have static, cardiant, antiarteriosclerotic, antiasthmatic and hyperteriosclerotic.
                                                                                                                                                                                                                                       1.
                                                                                                                                                                                                                                                                                                                                             ABX97157.
             Similarity
                                                                                                                                                                                                                                                                                  hypertension,
                                                                                                                                                                                                                                     Page 410; 1103pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-0332094P.
; 2001US-0337426P.
; 2001US-0338092P.
; 2001US-0337185P.
; 2002US-0345705P.
                                                                                                                                                                                                                                                                                                                                                                                       Rieger DK;
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Gusev V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-00092900
             35.7%;
                                                                                                                                                                                                                                                                                  polynuclectides, useful for preventing or treating with aberrant NOVX expression or activity e.g., atherosclerosis, cardiomyopathy or bronchial
                                                                                                                                                                                                                                     English.
Score 55; DB Pred. No. 22; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taupier RJ, Pena
n L, Miller CE, I
                             Length 403;
                                                                                                                                                                                                                                                                                                                                                                                                     Tchernev V;

h V, Liu Y,

Zhong H, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kekuda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEA,
                                                                                                                                                                                                and hypotensive
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Alsobrook JP;
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Matches
23-JAN-2002
                    ABB16658;
                                       ABB16658
                                                                                         118
                                                                                                                                 12;
                                      standard;
                                                                                          RRGLSALRGAAGLAWRIFLLLAVTLP 143
                                                                                                              RRGAGAARGRASWCWALALLWLAVVP 27
                                                                                                                                  Conservative
(first entry)
                                      protein;
                                         78
                                       A
                                                                                                                                   Indels
                                                                                                                                   0;
                                                                                                                                   Gaps
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0

system related polypeptide SEQ ID NO 5315.

17-JAN-2001; 2001WO-US001334.

16-AUG-2001

WO200159063-A2

Homo

sapiens.

neurological disease; infection;

nephrotropic;

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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
11-SEP-2000;
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05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
 21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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27-SEP-2000;
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29-SEP-2000;
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07-JUL-2000;
11-JUL-2000;
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11-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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01-SEP-2000;
2000US-020447P.
2000US-021513P.
2000US-021647P.
2000US-021647P.
2000US-021745P.
2000US-021745P.
2000US-022566P.
2000US-0225266P.
2000US-022575P.
2000US-023575P.
2000US-023575
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2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
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2000US-0180628P.
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2000US-0186350P
        02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
20-OCT-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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08-DEC-2000;
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08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
                                                    WPI; 2001-541565/
N-PSDB; ABA12984.
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      Nucleic acids encoding useful for preventing,
                                                                                                     Rosen
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17-NOV-2000;
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      3224 human nervous system antigen polypeptides, diagnosing and/or treating nervous system cancers
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aptamer; thioredoxin fusion aptamer; inhibitor; growth; cell viability; virulence; aptamer expression library; antibacterial agent; psoriasis; antiviral agent; human immune deficiency virus; protease inhibitor; cellular proliferation; cancer; autoimmune disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY43189 standard;
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      This sequence represents a toxic thioredoxin fusion aptamer, and was identified using the method of the invention. The method is for the identification of an aptamer (I) inhibiting either growth, viability or virulence of an organism, or the biological function of an essential
                                                                                                                                                                                                                New aptamers that inhibit growth, viability or virulence of organisms, potentially useful as antibacterial and antiviral agents.
                                                                                                                                                                                                                                                                                                                                                                         Mekalanos JJ,
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Best Local :
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                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutat responsible for genetic disorders or other traits and to asse
                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #1700
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                                                                                                                                                                      Claim 20; SEQ ID NO 32068; 103pp; English.
                                                                                                                                                                                                 biodiversity.
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42.1%;
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Pred. No. 3
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The

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$G96249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peroxidase-like activity; expression cassette; plant defence response; plant disease resistance; plant stalk strength; plant breeding; maize; plant; peroxidase.
                                                                                                                                                                              invention and all methods are useful for expression cassettes for modulating plant defence response, increasing plant disease resistance and increasing plant stalk strength. They can also be used in methods of selecting or breeding for plants with increased disease resistance. The present amino acid sequence represents a maize peroxidase protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New maize peroxidase nucleic acid molecule and polypeptide used expression cassettes for modulating plant defense response, inco
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16-JAN-2002; 2002US-00047825.
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                                                                                                      Sequence 346
                                                                                                                                                                                                                                                                                                            The present invention relates to a new nucleic acid molecule that encodes a polypeptide with peroxidase-like activity. The nucleic acid of the
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 87-88; 119pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                           plant disease resistance and increasing plant stalk strength
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                                                                       genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is custful for generating antibodies against it, detecting or quantitating a colypeptide in tissue, as molecular weight markers and as a food complement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders convolving abstrant protein expression or biological activity. The colypeptide and polymucleotide sequences have applications in colypeptide and polymucleotide sequences have applications in colypeptides, forensics, gene mapping, identification of mutations compossible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and camino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WIPO at the coloring format directly from WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also use in diagnostics as expressed sequence tags for identifying expressed
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23-AUG-2000; 2000US-00649167.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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RESULT 2 US-07-683-957B-2 ; Sequence 2, Applicat ; Patent No. 5310880 ; Patent No. 5310880 ; Patent No. 5310880 ; Patent No. 5310880 ; REPLICANT: Donah ; APPLICANT: Ragin ; APPLICANT: MacLe TITLE OF INVENTIC ; TITLE OF INVENTIC ; TITLE OF INVENTIC ; TITLE OF INVENTIC ; TUNDERS OF SEQUENC ; NUMBER OF SEQUENC ; CORRESPONDENCE AL ; CARDESSEE: St. STREET: 1100 I CITY: Washing! ; STATE: D.C. COUNTRY: U.S.; ; COMPUTER READABLI MEDIUM TYPE: ; MEDIUM TYPE:	Query Match Best Local Sin Matches 11; Qy 4 GP Db 13 GI	RESULT 1 US-09-621-976-60) ; Sequence 6090, ; Sequence 6090, ; Patcent NO. 663; ; Patcent INFORM; ; APPLICANT: Du APPLICANT: Du APPLICANT: OF APPLICANT: OF INTLE OF INVE FILE REFERENCY CURRENT FILIN CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; CURRENT FILIN ; NUMBER OF SEQ ; SOFTWARE: PAT ; SEQ ID NO 6090 ; LENGTH: 74 ; TYPE: PAT ; ORGANISM: HO US-09-621-976-60		28 29 47 29 31 46.5 32 46.5 33 46.5 36 46.4 46 39 46 46 46 46 39 46 46 46 46 46 46 46 46 46 46 46 46 46
2, Application US/07683957B 1, S310880 1. S310880 1. MANT: Donahoe, Patricia K. ANT: MacLaughlin, David T. ANT: MacLaughlin, David T. OF INVENTION: Purification of M llerian Inhibiting OF INVENTION: Substance OF SEQUENCES: 7 PONDENCE ADDRESS: ESSEE: Sterne, Kessler, Goldstein & Fox ETT: 1100 New York Avenue, N.W. ET D.C. TE: D.C. TTRY: U.S.A. 20005 100	34.4%; Score 53; DB 4; Length 74; similarity 39.3%; Pred. No. 1.6; ; Conservative 3; Mismatches 10; Indels 4; Gaps GAGAARGRASWCWALALLWLAVVP 27	11-976-6090 Ince 6090, Application US/09621976 NO. 6639063 NO. 6639063 LINFORMATION: CANT: Dumas Milne Edwards, J.B. CANT: Jobert, S. CANT: Jobert, S. CANT: Giordano, J.Y. SOF INVENTION: ESTs and Encoded Human Proteins. REFERENCE: GENSET:054PR2 NT APPLICATION UNMERR: US/09/621,976 ENT FILING DATE: 2000-07-21 ENT FILING DATE: 2000-07-21 STR OF SEQ ID NOS: 19335 JNO 6090 JNO 6090 STR: Patent.pm JNO 6090 11-976-6090	ALIGNMENTS	30.5 177 4 US-09-252-991A-24167 Sequence 24167, A 30.5 250 4 US-09-252-991A-24075 Sequence 24075, A 30.5 439 4 US-09-252-991A-13336 Sequence 13336, A 30.2 418 4 US-09-252-991A-18097 Sequence 10907, A 30.2 418 4 US-09-252-991A-17598 Sequence 40907, A 29.9 191 2 US-08-252-991A-28415 Sequence 4, Appli 29.9 193 4 US-09-252-991A-28415 Sequence 28415, Appl 29.9 200 4 US-09-252-991A-28054 Sequence 176, Appl 29.9 200 4 US-09-252-991A-28054 Sequence 176, Appl 29.9 335 4 US-09-570-8568-15 Sequence 176, Appl 29.9 335 4 US-09-252-991A-25031 Sequence 25031, A 29.9 560 4 US-09-252-991A-25031 Sequence 26787, A 29.9 576 4 US-09-252-991A-23246 Sequence 23246, A 29.5 263 4 US-09-252-991A-3311 Sequence 10, Appl 29.5 270 4 US-09-489-847-232 Sequence 311, Appl 29.5 273 4 US-09-489-847-232 Sequence 232, Appl

OPERATING SYSTEM:

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IS-07-683-957B-2
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15-09-252-991A-16705
                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MARC J. RUBENFIELD ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                   Sequence 19862, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
SEQ ID NO 16705
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Best Local Similarity
                                                                                                                               GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 466-0800
TELEPAX: (202) 83-8716
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                          -09-252-991A-19862
                  FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                      APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 170
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NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3060000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
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                                                                                                                                                                                                                                                                       108 RAAGATRRRPGWTCGANPRPCWSAAGSW 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                             3 RGAGAARGRASW-----
                                                                                                                                                                                                                                                                                                                                                                        Similarity
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  US 60/074,788
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Pred. No. 15;
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Pred. No. 5.1;
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19862
; LENGTH: 217
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                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER APPLICATION NUMBER: 60/049,375
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SEQ ID NO 22
LENGTH: 85
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Patent No. 6585975
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TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: Vaccination against helicobacter infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/431,705
CURRENT FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                      APPLICANT: Young et al. TITLE OF INVENTION: 207 Human Secreted Proteins
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TYPE: PRT
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                                                    EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PZ007P1
                                                                                                                              EARLIER APPLICATION NUMBER: 60/048,881
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ORGANISM: Escherichia
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                  FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,020
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 9; Conserv
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Londono-Arcila, Patricia
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  1997-06-06
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Pred. No. 6.6;
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Pred. No. 3.
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SEQ ID NO 274
LENGTH: 88
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                                                                                                                       NUMBER OF SEQ ID NOS: 1227
                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/094,657
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
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; LOCATION: (88)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-274
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US-09-170-496D-290
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          PRIOR FILING DATE: 1998-07-31
PRIOR APPLICATION NUMBER: 60/106,300
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/110,906
PRIOR FILING DATE: 1999-12-04
PRIOR FILING DATE: 1999-12-04
PRIOR PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 60
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Best Local Similarity
Matches 13; Consert
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Matches
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CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/364,425B
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/094,879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: No. 6555339-Endogenous,
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APPLICANT: Chalme
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                                                                                                                                                                                     FILE REFERENCE: Aren0047
                                                                                                                                                                                                    APPLICANT: Lowitz, Kevin P.
APPLICANT: Chen, Ruoping
TITLE OF INVENTION: Endogenous, Constitutively Activated G
                                                                                                                                                                                                                                                                                                    APPLICANT: Behan, Dominic
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TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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9; Conserv
PatentIn version 3.1
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                                                                                                                                                                                                                                                                  Liaw, Chen W.
                                                                                                                                                                                                                                                                                   Chalmers, Derek T
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ilarity 52.9%;
Conservative
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Pred. No.
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Pred. No. 3.
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RESULT 10

15-09-125-991A-26303

; Sequence 26303, Application US/09252991A

; Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLILING DATE:
FILING DATE:
CLASSIFICATION: 530
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000-3500
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 1310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDLIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SMITH, DOU APPLICANT: MAO, JEN-I
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                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                                                          163 MRENRGSQERVGARLLYQWRWSLATLWFTTV 193
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MASSACHUSETTS
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                                                                                                                                                                            32.8%;
ilarity 38.7%;
Conservative
                                                                                                                                                                                                                                                                        MYCOBACTERIUM TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                           linear
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52.9%;
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Pred, No. 10;
2; Mismatches
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US-09-252-991A-27451
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APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/081,563
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US-09-247-155-98
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LENGTH: 127
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TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 27451, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                            Patent No. 631292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 27451
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 286
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8; Conserv
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Pred. No. 17;
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ESULT 14
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Best Local Similarity 45.0%;
Matches 9; Conservative
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: INTEL OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 98
                                                                                                                                                                                                                                                              Sequence 25696, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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SEQ ID NO 31079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31079, Application US/09252991A
Patent No. 6551795
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EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
SEQ ID NO 25696
                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 199-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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SOFTWARE: Patent.pm
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ORGANISM: Homo sapiens
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Pred. No. 13;
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Pred. No. 6.1;
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Query Match
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Job time : 3.17778 secs
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US-09-252-991A-31234
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SEQ ID NO 31234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 31234, Application US/09252991A Patent No. 6551795
                                                                                                                                             Matches
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                         Local Similarity les 14; Conserv
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                                                                       686 LRAGQGQAEGRVTLRFDNGVAWDTALQLSELNPAYWVAELPG 727
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(without alignments)
1368.675 Million cell updates/sec
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12 US-10-653-595-126
13 US-10-010-050A-2
13 US-9-397-945-126
12 US-9-397-945-126
12 US-9-811-284-167
15 US-10-156-761-1153
18 US-10-156-761-153
18 US-10-080-170-198
19 US-10-080-170-198
10 US-10-080-170-198
11 US-10-156-761-10933
12 US-10-047-825-11
12 US-10-221-278-727
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Sequence 2, Appli
Sequence 126, App
Sequence 2, Appli
Sequence 126, App
Sequence 167, App
Sequence 269, App
Sequence 11538, App
Sequence 240, App
Sequence 198, Appli
Sequence 198, Appli
Sequence 19933, App
Sequence 10933, Appli
Sequence 10933, Appli
Sequence 107, Appli
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US-10-230-434-80	-219-07	-10-227-883-	-10-227-873-	-10-218-8	-10-216-159	-10-230-414-	18-631-	0-230-338-	-10-230-	-10-227-884-	-10-232-224-	0-232-	-10-219-535-8	9-863-776-6	9-863-776-	09-901-812	9-759-056-	9-863-776-	09-863-776-6	09-901-81	09-759-056	-60	-10-104-047-	-09-863-776-	US-10-424-599-167251	-10-424-599-20728	-10-282-122A-	-738-626-47	US-10-291-172-727
Sequence 80, Appl	Φ	equence 80,	e 80,	equence 80,	e 80,	equence 80,	e 80,	equence 80,	e 80,	equence 80,	e 80,	equence 80,	80,	equence 67,	9	equence	2,	e 3(e 68, App	equence 5, Ap	ۍ ت	28	equence 230	69, 2	equence 167	equence 2072	e 50396	quence 4771,	Sequence 727, App

ALIGNMENTS

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US-10-653-595-126; Requence 126, Application US/10653595; Publication No. US20040048304A1; GENERAL INFORMATION: APPLICANT: Ruben et. al. APPLICANT: Ruben et. al.
                                                                                                           RESULT 2
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                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapien US-09-122-383-2
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US-09-122-383-2
                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1998-07-24
EARLIER APPLICATION NUMBER: 60/053,613
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
RITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38
CURRENT APPLICATION NUMBER: US/09/122,383A
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Conservative 0
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Pred. No. 6e-11;
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PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: US 09/397945 CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03

FILE REFERENCE: PZ027P1C1

DB 13;

Length

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (246)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
JS-10-653-595-126
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; LENGTH: 346
; TYPE; PRT
; ORGANISM: Homo sapien
US-10-010-050A-2
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NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 126
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/10010050A Publication No. US20020173624A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/010,050A CURRENT FILING DATE: 2002-03-26 PRIOR APPLICATION NUMBER: US 09/122,383 PRIOR FILING DATE: 1998-07-24 PRIOR APPLICATION NUMBER: US 60/053,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
                                                                                                                                PRIOR FILING DATE: 1997-
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                            APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sheppard, Paul APPLICANT: Gilbertson, De
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                                                                                                                                                                                                                                                                                       FILE REFERENCE: 97-38C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Kaa equals any of the naturally occurring L-amino acids
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FILING DATE: 1998-03-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/080,314 FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/078,578
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28; Conserv
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Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 28; Conservative 0; Mismatches
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Publication No.
                                                                              Query Match 100.0%; Score 154; DB 1
Best Local Similarity 100.0%; Pred. No. 6e-11;
Matches 28; Conservative 0; Mismatches
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LENGTH: 347
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CURRENT FILING DATE: 1999-09-17
                                                                                                                                                                                                        LOCATION: (246)
OTHER INFORMATION: )
NAME/KEY: SITE
LOCATION: (347)
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PRIOR APPLICATION NUMBER: 60/078,577
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,563
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
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PRIOR FILING DATE: 1999-03-18
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PRIOR APPLICATION NUMBER: 60/078,581
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                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
LOCATION: (242)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                NAME/KEY: SITE
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                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-04-01
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  MRRGAGAARGRASWCWALALLWLAVVPG 28
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o. US20030065139A1
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CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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ORGANISM: Homo sapiens
S-09-811-284-167
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CURRENT FILING DATE: 2001-03-16
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                                       PRIOR APPLICATION NUMBER: 09/633,870 PRIOR FILING DATE: 2000-09-15
                                                                                                                                                                                                                                                               APPLICANT: Hyseq, Inc.
APPLICANT: Tang et al.
TITLE OF INVENTION: No. US20030232054Alel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-017 (785)
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                       NUMBER OF SEQ ID NOS:
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FastSEQ
for Windows Version 3.0
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; TYPE: PRT
; ORGANIZM: Streptomyces avermitilis
US-10-156-761-11538
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US-10-156-761-11538
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SEQ ID NO 11538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 269
LENGTH: 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11538, Application US/10156761 Publication No. US20030119018A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                   SOFTWARE: PatentIn version 3.1
SEQ ID NO 240
                                                                                                                                                                                                                                                                                                                           Patent No. US2002017
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.3%; Score 59; DB Best Local Similarity 29.5%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                     CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
                                                                                                                                                                                     APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghing
TITLE OF INVENTION: Compositions and Methods Relating
FILE REFERENCE: DEX-0291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                   APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 12
TYPE: PRT
               LENGTH:
TYPE: PR
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 RGAGSSRTKLYATKNLTELIGVYGSRYGGDKSSWSWAGGLIWLA 210
                                                                                                                                                                                                                                                                                                                                                               240, Application US/09989920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 RGEGETWGRVTMTKLAQWLWGLAILGSTWVALTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RGAGAAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 RGAGAARGR-----ASWCWALALL---WLAVVPG 28
                                                                                                                                                                                                                                                                   Recipon, Herve
Chen, Sei-Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                               20172957A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 7.8; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59.5;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GRASWCWALALLWLA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
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                                                                                                                                                                                                               to Lung Specific Genes and Prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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JS-09-989-920-240

3 RGAGAARGRASWCWALALLWLAVV

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; LENGTH: 214
TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-10-080-170-198
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 198, Application US/10080170 Publication No. US20030129601A1 GENERAL INFORMATION: APPLICANT: COLE, S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 8
LENGTH: 19608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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  Matches
                                                                                                                                                                            SEQ ID NO 198
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                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/084,846A CURRENT FILING DATE: 2003-02-25 PRIOR APPLICATION NUMBER: PCT/EPO1/09815 PRIOR FILING DATE: 2001-08-24 PRIOR APPLICATION NUMBER: DE 101 09 166.4 PRIOR APPLICATION NUMBER: DE 101 09 166.4 PRIOR FILING DATE: 2001-02-25 NUMBER OF SEQ ID NOS: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: WEITNAUER, GABRIELE
APPLICANT: MUHLENNEG, AGNES
APPLICANT: TREFZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
FILE REFERENCE: 1974-005
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/080,170 CURRENT FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                                                                APPLICANT: COLE, S.T.
TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1. OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 38.7 nes 12; Conservative
                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2876 RRAAVTPGARGRVEWCGPVSGVWLCAPP 2903
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  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGGAGAGSWVWMGGWGGGAGALWVAVVGG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGAARGRASWCW-----ALALLWLAVVPG 28
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Conservative
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38.7%;
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                       36.4%; Score 56;
41.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 57; DB 15; Length 19608; Pred. No. 1.2e+03; 3; Mismatches 11; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 58; DB 9; Pred. No. 17;
    Mismatches
                                           DB 14; Length 214;
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      Indels
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CURRENT APPLICATION NUMBER: US/10/092,900A
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: USSN 60/274,322
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/283,675
PRIOR APPLICATION NUMBER: USSN 60/283,675
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR APPLICATION NUMBER: USSN 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/325,681
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: USSN 60/304,354
PRIOR APPLICATION NUMBER: USSN 60/304,354
PRIOR APPLICATION NUMBER: USSN 60/304,354
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR APPLICATION NUMBER: USSN 60/279,995
PRIOR APPLICATION NUMBER: USSN 60/279,995
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; TYPE: PRT ; ORGANISM: Homo sapiens US-10-092-900A-300
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                                                          Remaining Prior Applic
NUMBER OF SEQ ID NOS:
SEQ ID NO 300
LENGTH: 403
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APPLICANT:
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                                                                                                                                               PRIOR APPLICATION NUMBER: USSN 60/287,424 PRIOR FILING DATE: 2001-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: No. US20040043382Alel Proteins and Nucleic
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                                                                                                                                                                                        APPLICATION NUMBER: USSN 60/294,899 FILING DATE: 2001-05-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leite, Mario W. Zhong, Haihong Alsobrook, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patturajan, Meera
Gangolli, Esha A.
Vernet, Corine A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zerhusen, Bryan D.
Gusev, Vladimir Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lepley, Denise M.
Rieger, Daniel K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tchernev,, Veliz
Fernandes, Elma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spaderna, Steven K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerlach,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10092900A
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                                                                                                                           Application data removed -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stacie J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Valerie
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                                                                                                                                See File Wrapper or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acids Encoding
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Same

Query Match Best Local, Matches 1

Local Similarity

35.7%;

Score 55; DB Pred. No. 73;

DB 12;

Length 403;

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APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
                                                                                       ORGANISM: Zea mays
IS-10-047-825-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-10-156-761-10933
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LENGTH: 160
TYPE: PRT
    Best Loc
Matches
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APPLICANT: Duvick, Jon
APPLICANT: Maddox, Joy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                             Query Match
                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10 LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10047825 Publication No. US20030017566A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                         APPLICANT: Navarro Acèvedo, Pedro
APPLICANT: Simmons, Carl R.
TITLE OF INVENTION: Maize Peroxidase Genes and Their Use for
TITLE OF INVENTION: Improving Plant Disease Resistance and Stalk Strength
FILE REFERENCE: 35718/242052
CURRENT APPLICATION UNMBER: US/10/047,825
CURRENT FILING DATE: 2002-01-16
                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/262,595 PRIOR FILING DATE: 2001-01-18
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces avermitilis
/ Match 34.4%;
Local Similarity 50.0%;
nes 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AARGRASW--CWALALLWLAVVPG 28
                                                                                                                                                                                                                                                                                                                                                                                                                              Maddox, Joyce
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  Score 53; DB 12;
Pred. No. 1.1e+02;
2; Mismatches 2;
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Pred. No.
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                                             Length 346;
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      Indels
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US-10-221-278-727
Sequence 727, Application US/10221278
Publication No. US20040034208A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/693,267
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/665,363
PRIOR FILLING DATE: 2000-09-19
PRIOR FILLING DATE: 2000-09-19
PRIOR FILLING DATE: 2000-07-14
PRIOR FILLING DATE: 2000-07-14
PRIOR FILLING DATE: 2000-06-17
PRIOR FILLING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILLING DATE: 2000-05-19
PRIOR FILLING DATE: 2000-05-19
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Matches
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PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 752
SEQ ID NO 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 55731, Application US/10425114 Publication No. US20040034888A1
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5331)B
CURRENT EPPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 21272-045
CURRENT APPLICATION NUMBER: US/10/221,278
CURRENT FILING DATE: 2002-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hyseq, Inc
TITLE OF INVENTION: No. US20040034208Aiel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
OTHER INFORMATION: Xaa = any amino acid or nothing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: UC-ZMFLB73111F11_FLI.pep
                       NAME/KEY: misc_feature LOCATION: (1)...(199)
                                                              FEATURE:
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                                                                                                                                ENGTH: 199
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12; Conserv
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154
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1331.883 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

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A CONTRACT CAN TANCE	1	T-cell receptor qa	conserved hypothet	probable competenc	probable integral	μ.	ct	ankB protein VC158	prot		O	ical mem	ABC transporter tr	transporter	۳				Ϋ́	collagen, cornea-s	ferric reductase (probable intercell	mullerian inhibiti	hypothetical prote		conserved hypothet	probable integral	-	fate transpor	Description

ALIGNMENTS

R.Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lia A;Title: Genome sequence of Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: C84390 片 C84390 sulfate transport system permease protein [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: C84390 Š A;Gene: cysT1 A;Cross-references: GB:AE004437; NID:g10581803; PIDN:AAG20487.1; GSPDB:GN00138 C;Genetics: A; Molecule type: DNA A; Residues: 1-606 <STO> A; Status: preliminary RESULT 1 Matches Query Match Local 508 RALGASRGRALWDVELPLVWPGVVAG 533 l Similarity 14; Conserv w RGAGAARGRASWCWALALLWLAVVPG 28 Conservative 42.9%; 53.8%; 2 Score 66; DB 2; Pred. No. 0.31; Mismatches 10; Length 606; Indels °, Gaps 0;

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95941 conserved hypothetical membrane protein, paralogue of Y20848 SMb21292 [imported] - Sinorl
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95941

A;Status: preliminary A;Molecule type: DNA

A; Residues: 1-412 < KUR>

A; Gross-references: GB:AL591985; PIDN:CAC49196.1; PID:g15140681; GSPDB:GN00167

A; Experimental source: strain 1021, megaplasmid pSymB

R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A; Authors: Kain, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A; Authors: Kain, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Weils, D.H.; Wong, K.; Yeh, K.(

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A; Cross-references: Granusca, C., Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Ariones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Brento, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.B.; Laigu hado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marrins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; M.Yaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.G.; de Oliveira, R.C.; Palmieri, D.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.G.; de Silva, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A. da Silveira, M.A.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A. da Silveira, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
1;Reference number: A82515; MUID:20365717; PMID:10910347
1;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Accession: F82729
Ranonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein XF1054 [imported] - Xylella fastidiosa (stra
};Species: Xylella fastidiosa
};Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
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I;Experimental source: cosmid B1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;Gene: SMb21292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Accession: F82729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: MLCB1243.07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                               );Cross-references: GB:AE003942; GB:AE003849; NID:g9105990; PIDN:AAF83864.1; GSPDB:GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2968c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; translated
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-214 <PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTSAIARGIYQWRWSIATLWFITV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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41.7%;
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Pred. No. 1.9;
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C;Accession: AI2860

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Jerage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
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                                                                                                                                                                                                                   A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H97637
                                                                                                                                                                                                                                                                           R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Science 294, 2323-2328, 2001
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A;Map position: circular chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 A;Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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                                                                                                                                       A; Cross-references: GB: AE007869; PIDN: AAK88057.1;
                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-428 < KUR>
                                                                                                                                                                                                A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                      C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: H97637
                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein AGR C 4211 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                       H97637
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nilarity 47.4%;
Conservative
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nilarity 29.6%;
Conservative
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                    34.4%;
29.6%;
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Pred. No.
7;
                  Score 53; DB pred. No. 12;
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McClella
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AARGRASWCWA----

-LALLWLAVVP 27

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Comment: This protein is homologous to the beta transforming growth factor, inhibin al hese sequences. All of these proteins are biologically active as disulfide-linked dimer (Comment: Although it does not compete with EGF for receptor binding sites, MIS can inhibin (Superfamily: inhibin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comment: This glycoprotein, produced by the Sertoli cells of the testis, tissues of Mullerian duct origin. Other roles for this protein in gonadal er duct regression and in the adult ovary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n, K.L.; Ragin, R.C.; Manganaro, T.F.; MacLaughlin, D.T.; Donahoe, P.K. ell 45, 685-698, 1986
Fittle: Isolation of the bovine and human genes for Muellerian inhibiting substance; Reference number: A90879; MUID:86218082; PMID:3754790
ESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ullerian inhibiting factor precursor -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Keywords: cytotoxin; glycoprotein; gonadal differentiation; testis; 1-19/Domain: signal sequence #status predicted <SIG>,20-24/Domain: propeptide #status predicted <PRO>,25-575/Product: mullerian inhibiting factor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           robable intercellular signal transducer or transmitter Fz-1 - rat;
Species: Rattus norvegicus (Norway rat);Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;78,344/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                            Superfamily:
                                                                                                                                                                                                                                                                                Experimental source: UMR 106 osteosarcoma cell line Note: sequence extracted from NCBI backbone (NCBIP:120154)
                                                                                                                                                                                                                                                                                                                                                                                                                           Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino, Biol. Chem. 267, 25202-25207, 1992
Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely expresses. Reference number: A45054; MUID:93094228; PMID:1334084
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Residues: 15-575 <CA2>
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                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                            Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A45054
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                                                                                                                                                                                                                                                                                                                                                        Molecule type: nucleic acid
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                                                                                                               AGAARGRA-SWCWA---LALLWLAVVP 27
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                                                                                                                                                                                                                                                            fruit fly
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Pred. No. 19;
4; Mismatches
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Pred. No.
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RESULT 10
A38587
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A;Title: Ferric reductase of Saccharomyces cerevisiae: Molecular characterization, role i A;Reference number: S30075; MUID:92237270; PMID:1570306
A;Accession: S30075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence revision 28-May-1993 #text_change 17-Mar-2000
C;Accession: S30075; S48565
R;Dancis, A.; Roman, D.G.; Anderson, G.J.; Hinnebusch, A.G.; Klausner, R.D.
Proc. Natl. Acad. Sci. U.S.A. 89, 3869-3873, 1992
                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-174,'X',176-233,'X',235-344,'X',346-408,'X',410-499,'X',501-876,'X',878-114
A;Cross-references: GB:M60172
                                                                                                                                                                                                                                                                                                        R;Marchant, J.K.; Linsenmayer, T.F.; Gordon, M.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 1560-1564, 1991
A;Title: cDNA analysis predicts a cornea-specific colla
A;Reference number: A38587; MUID:91142213; PMID:1705041
A;Accession: S16501
                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Gallus gallus (chicken)
C;Date: 14-Feb-1992 #sequence_revision 15-Aug-1997 #text_change 15-Sep-2003
C;Accession: S16501; A38587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: ferric reductase C; Keywords: oxidoreductase; tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Pauley, A. submitted to the EMBL Data Library, September 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ferric reductase (EC 1.6.99.-) FRE1 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein L8167.2; protein YLR214w
                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-1146 < MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;359-375/Domain: F;531-547/Domain:
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A; Residues: 1-686 < DAN >
                                                                                                                               C; Keywords: cornea
                                                                                                                                                                                                                  A;Cross-references: EMBL:M60172; NID:g211609; PIDN:AAA48703.1; PID:g211610
A;Accession: A38587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collagen, cornea-specific -
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#status predicted <TM3>
#status predicted <TM4>
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                                           Pred. No. 45;
2; Mismatches
                                                                Score 51.5;
Pred. No. 49
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Pred. No. 29;
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-МАЦАЦЬ--МЦАVV 26
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, 3. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.3.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230

A;Accession: E70671
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\(); Experimental source: strain 1021, megaplasmid pSymB
\(); Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; F.sher, R.F.; L.; Hyman, R.W.; Jones, T.
\(); Hyman, R.W.; Jones, T.
\(); Li, Hyman, R.W.; Jones, T.
\(); Science 293, 668-672, 2001
\(); Alphan, M.D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, nebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
\(); Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
\(); Reference number: A96039; MUID:21368234; PMID:11474104
C; Superfamily: Mycobacterium tuberculosis hypothetical
                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-210 <SMI>
                                                                                                                                                                                                                                                                                                  A, Experimental source: strain H37Rv
R; Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, September 1994
A; Description: Mycobacterium tuberculosis cosmid tbc2
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-210 <COL>
A;Residues: 1-210 <COL>
A;Cross-references: GB:Z83018; GB:AL123456; NID:g3261671;
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A;Molecule type: DNA
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rroc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
k;Title: The complete sequence of the 1,633-kb pSymB megaplasmid from the N2-fixing endc
k;Reference number: A95842; MUID:21396508; PMID:11481431
                                                          A; Gene: Rv2968c
                                                                                                                       A; Cross-references:
                                                                                                                                                                                                                                        A; Accession: S73054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Rv2968c - Mycobacterium tuberculosis (strain H37RV)
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\;Residues: 1-410 <KUR>
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                                                                                                                       PIDN:AAA50949.1;
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      A;Status: preliminary
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hypothetical C;Species: Rai C;Date: 31-Ma:
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A;Cross-references: GB:M15527; NID:g206910; C;Superfamily: rat hypothetical protein SH
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                                                                                       hypothetical protein BH2519 [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: G83964
                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-163 <SMI>
A;Cross-references: EMBL:U00022; NID:g467164; PIDN:AAA17338.1; PID:g467180
C;Superfamily: Mycobacterium leprae hypothetical protein L308_F1_25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein L308 F1_25 - Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #te:
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                 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Nacleic Acids Res. 28, 4317-4331, 2000

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium A;Reference number: A83650; MUID:20512582; PMID:11058132
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C; Accession: S73039
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A; Reference number: A83650;
A; Accession: G83964
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| Molenite type: NM. | Residues: 1221 | ACTOS | Férences: GB:APO01515; GB:BA000004; NID:g10174886; PIDM:BAB06238.1; GSPDB:GNOC | EXPERIMENTAL | ACTOS | GB:APO01516; GB:COST | GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516; GB:APO01516;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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-!- FUNCTION: Not known!- SUBCELLULAR LOCATION: Lysosomal!- TISSUE SPECIFICITY: Ubiquitous!- DISEASE: Defects in CLN5 are the cause of Finnish variant late- infantile neuronal ceroid lipofuscinosis (VLINCL) [MIM:256731]; also known as ceroid lipofuscinosis neuronal 5 (CLN5) VLINCL is a fatal childhood neurodegenerative disease characterized by progressive visual and mental decline, motor disturbance, epilepsy and behavioral changes. The first symptom is motor clumsiness, followed by progressive visual failure, mental and motor deterioration and later by mycolonia and seizures. NOTE-Neural Ceroid Lipofuscinoses mutation db; WWW#=http://www.ucl.ac.uk/ncl/CLN5.html"	CLNS HUMAN STANDARD; O7550; 15-DEC-1998 (Rel. 37, La 15-DEC-1998 (Rel. 37, La 10-OCT-2003 (Rel. 42, La Ceroid-lipofuscinosis ne CLNS. Ceroid-lipofuscinosis ne CLNS: Eukaryota; Metazoa; Chor Mammalla; Eutheria; Prim NCBI TaxID=9606; Il TaxID=9606; Il TSUES-Fetal brain; MEDLINE=98324783; PubMed Savukoski M., Klockars I TISSUE-Fetal brain; MEDLINE=98324783; PubMed Savukoski M., Klockars I Peltonen L.; "CLNS, a novel gene enco in Finnish variant late Nat. Genet. 19:286-288(1 [2] SUBCELLULAR LOCATION, AN MEDLINE=21968572; PubMed ISOSOmppi J., Vesa J., "Lysosomal localization protein.";	

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or send a
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Bacteria; Proteobacteria; Betaproteobacteria; Bur
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CRCB OR RSC1333 OR RS02855.
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                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                             MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                        STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                  SEQUENCE
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InterPro; IPR003691; C
Pfam; PF02537; CRCB; 1
TIGRFAMS; TIGR00494; c
                                                                                                                  use by non-profit institutions as long as modified and this statement is not removed. I
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                                                                         EMBL; AL646064; CAD15035.1; -.
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                     Transmembrane;
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P:cell growth and/or maintenance; TAS
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SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1;
PROSITE; PS00250; TGF BETA 1;
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23-OCT-1986 (Rel. 02, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Muellerian inhibiting factor precursor (MIS)
(AMH) (Mullerian inhibiting substance).
                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheung A., Ninfa E.G., Frey A.Z., Gash D.J., Chow E.P., Fisher R., Bertonis J.M., Torres G., Wallner B.P., Ramachandran K.L., Ragin R.C., Manganaro T.F., McLaughlin D.T., Donahoe P.K., "Isolation of the bovine and human genes for Mullerian inhibiting
                                           CHAIN
                                                                                                                                                                         Pfam; PF04709; AMH_N; 1.
Pfam; PF00019; TGF-beta; 1.
PRINTS; PR00438; GFCYSKNOT:
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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InterPro; IPR002400; GF_Cy
InterPro; IPR001839; TGFb.
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Bovidae; Bovinae; Bos.
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FUNCTION: THIS GLYCOPROTEIN,
TESTIS, CAUSES REGRESSION OF
TO INHIBIT THE GROWTH OF TUMO
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een the Swiss Institute of Bio:
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E.P., Fisher R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             by and
                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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on of the EGF
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OF MUELLERIAN
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Q08463;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-CT-2003 (Rel. 47, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley; TISSUE=Osteosarcoma, MEDLINE=93094228; PubMed=1334084; Chan S.D.H., Karpf D.B., Fowlkes M.E., Hooks M. Vuong V., Bambino T., Liu M.Y.C., Arnaud C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologs in a G-protein-dependent manner.";
Curr. Biol. 9:695-698(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sheldahl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99324245; PubMed=10395542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUPLING TO BETA-CATENIN PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
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                                                                                                                                                                                    SUBCELLUTAR LOCATION: Integral membrane
TISSUE SPECIFICITY: Widely expressed. Mo
liver, uterus, ovary and heart. Lower le
intestine. Extremely low in calvaria, ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                  TISSUE SPECIFICITY: Widely expressed. Most abundant in kidney, liver, uterus, ovary and heart. Lower levels seen in brain and intestine. Extremely low in calvaria, mammary glands and testis. DEVELOPMENTAL STAGE: Expressed predominantly in neonatal tissues,
                                                                                the Wnt/beta-catenin signaling pathway DOMAIN: The FZ domain is involved in b
                                                                                                                         at lower levels in adult.

DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation
  SIMILARITY:
                                           SIMILARITY:
                                                                                                                                                                                                                                                                                                transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8 induces expression of beta-catenin
                                                                                                                                                                                                                                                                                                                                                                GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Wnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                r. Biol. 9:695-698(1999).

FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors are compled to the beta-catenin canonical signaling pathway, while the activation of dishevelled proteins, inhibition of leads to the activation of dishevelled proteins inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homologs of the Drosophila polarity gene frizzled (fz) are widely essed in mammalian tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41
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Contains 1 frizzled (FZ) domain
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                                      Belongs to the Fz/Smo G-protein
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Pred. No. 11
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N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       γď
                                      coupled receptor
                                                                                with Wnt ligands
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                                                                                    01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ferric reductase transmembrane component 1 precursor (EC 1.16.1.7)
                                                                                                                                                                                                                                                 SITE
CARBOHYD
CARBOHYD
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SMART; SM00063; FRI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (So or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secre
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Pred. No. 14;
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

MEDLINE=92237270; PubMed=1570306;

Roman D.G.,

Anderson

G.J.,

Hinnebusch A.G.,

Klausner

Α.,

STRAIN=F113; SEQUENCE FROM N.A. NCBI_TaxID=4932; (Ferric-chelate reductase 1). FRE1 OR YLR214W OR L8167.2.

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R Germonline; 1422/6; -.

R Germonline; 1422/6; -.

R Germonline; 1422/6; -.

R GD; S0004204; FRE1.

R GO; G0:0005886; C:plasma membrane; IDA.

R GO; G0:0005896; F:ferric-chelate reductase activity; IDA.

R GO; G0:0006926; P:copper ion import; IDA.

R GO; G0:0015677; P:copper ion transport; IDA.

R GO; G0:0016826; P:iron ion transport; IDA.

R InterPro; IPR002916; Ferric reduct.

R Pfam; PF01794; Ferric reduct; 1.

Ovidoreductase; Electron transport; Transmembrane; Iron transport of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the compani
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RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,

RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W.,

RA Johnston M., Hillier L., Riles L., Dubois E., Duesterhoeft A.,

RA Johnston M., Belius H., Dubois E., Duesterhoeft A.,

RA Johnston M., Floeth M., Goffeau A., Hebling U., Heumann K.,

RA Johnston M., Floeth M., Goffeau A., Hebling U., Heumann K.,

RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

Mueller Auer S., Nentwich U., Obermaier B., Firavandi E., Pohl T.M.,

RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,

Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,

RA Vierendeels F., Voet M., Volkaert G., Voss H., Wambut R., Wedler E.,

Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.,

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
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Klausner R.D.;
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uptake.

capalytic activity: NADH + 2 Fe(3+) = NAD(+) + 2 Fe(2+).

CCFACTOR: FAD (Probable).

SUBCELLULAR LOCATION: Integral membrane protein.

INDUCTION: BY IRON DEPRIVATION. REPRESSED BY IRON UPTAKE
SIMILARITY: Belongs to the FRE / CYBB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          participate in the transport of electrons from cytoplasm to extracellular substrate (ferric ion) via FAD and heme intermediates. May also participate in Cu(II) reduction and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M86908; AAA34608.1;
U14913; AAB67424.1;
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Dolichol-phosphate mannosyltransferase subunit 3 (Dolichol-phosphate mannose synthase subunit 3) (Dolichyl-phosphate beta-D-mannosyltransferase subunit 3) (Mannose-P-dolichol synthase subunit 3)
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                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Science 235:1514-1517(1987).

-I- FUNCTION: May be involved with expression. It is not known if
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EMBL; AF312922; AAK28487.1;
EMBL; AF312923; AAK28486.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entitles requires a license and for comments or the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the service of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPM1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fransmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 605951; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate tumor invasion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO J. 19:2475-2482(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20296673; PubMed=10835346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the DPM3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthase complex. SUBUNIT: Composed of three subunits; DPM1, DPM2 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Associated with DPM1 via its C-terminal its N-terminal portion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Stabilizer subunit of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=1; Synonyms=Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthase
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IsoId=Q9P2X0-2; Sequence=VSP
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DPM2 and DPM3.";
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                                                                                                                                                                                                                                                                                       ASWCWALALL---WLAVVPG
                                                                                                                                                                                                                             AQWLWGLAILGSTWVALTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 AA;
                                                                                                                                                                                                                                                                                                                                                        Conservative
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57
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45.0%;
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Pred. No. 5
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.R., Casavant T.L., Scheetz T.E.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci p., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
VIllalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J. Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J. M., Salska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
RT Toco. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The neuronal ceroid lipofuscinoses in human EPMR and mnd mutant mice are associated with mutations in CLN8.";
Nat. Genet. 23:233-236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A., VARLELL.
SEQUENCE FROM N.A., VARLELL.
Lonka
                                                                                                                                                                                                                                                                                                                                                     resident of the endoplasmic reticulum.";

Hum. Mol. Genet. 9:1691-1697(2000).

-!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplamic reticulum and ER-Golgi intermediate compartment (ERGIC).

-!- PTM: Does not seem to be N-glycosylated.

-!- DISEASE: Defects in CLN8 are a cause of progressive epilepsy with mental retardation (EPMR) [MIM:600143]; also known as neuronal ceroid lipofuscinosis type 8 and Northern epilepsy. EPMR is an autosomal recessive disorder characterized by normal early development, onset of generalized seizures between 5 and 10 years,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ranta S., Zhang Y., Ross B., Lonka L., Takkunen E., Messer A., Sharp J., Wheeler R., Kusumi K., Mole S., Liu W., Soares M.B., Bonaldo M.F., Hirvasniemi A., de la Chapelle A., Gilliam T.C., Lehesjoki A.-E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutere
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20320699; PubMed=10861296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION, AND MUTAGENESIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lonka L., Kyttaelae A., Ranta S., Jalanko A., Lehe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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10-OCT-2003 (Rel.
                                                                                                                                                                                                                                        and subsequent progressive mental retardation. Biochemically, disease is characterized by the intracellular accumulation of hydrophobic material, mainly ATP synthase subunit C. SIMILARITY: Contains 1 TLC (TRAM/LAG1/CLN8) domain. DATABASE: NAME=NCL CLN8;
                                                                                                                                                                                                NOTE=Neural Ceroid Lipofuscinoses mutation db; WWW="http://www.ucl.ac.uk/ncl/CLN8.html".
                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
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42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT EPMR GLY-24, AND VARIANT ALA-155
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283-LYS-LYS-284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehesjoki A.-E.
rane protein is
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modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch). the European Bioinformatics Institute. The use by non-profit institutions as long

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PEXD
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Best Local
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EMBL; AF123758; AAF13116.1; -.
EMBL; AF123759; AAF13117.1; -.
EMBL; AF123750; AAF13118.1; -.
EMBL; AF123761; AAF13119.1; -.
EMBL; BC007725; AAH07725.1; -.
                                                                                                                                                                                                                                 Q19951;
Q19951;
15-DEC-1998 (Rel. 37, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable peroxisomal membrane protein PEX13 (
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This
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                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Endoplasmic reticulum; Neuronal Disease mutation; Polymorphism; Epilepsy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GG; GO:0005793; C:endoplasmic reticulum; TAS. GO; GO:0005793; C:ER-Golgi intermediate compa GO; GO:0016021; C:integral to membrane; TAS. GO; GO:0007399; P:neurogenesis; TAS.
                                                                                           Waterston R.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                 REVISIONS
                                                                                                                                     Submitted
                                                                                                                                              Pauley A.
                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                       NCBI_TaxID=6239;
                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                  Similarity).
SUBCELULAR LOCATION: Integral meml similarity).
SIMILARITY: Contains 1 SH3 domain.
                                                           FUNCTION: Component of the peroxisomal translocation machinery with PEX14 and PEX17. Functions as a docking factor for the predominantly cytoplasmic PTS1 receptor (PAS10/PEX5) (By
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copyright.
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Pred. No. 17;
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N -> S (IN REF. 2)
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TLC.
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/FTId=VAR_013174.
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P74055;
30-MAY-2000
between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-mib.ch).
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DOMAIN
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Bacteria; Cyanobacteria; Chroococca
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Peroxisome; Transport; Protein
DOMAIN 192 LU
TRANSMEM 193 213 PC
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                                                                                                                                              This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1148;
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LNT OR SLR0819.
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rabata
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InterPro; IPR001452; SH3.
                                                                                                                                                                                                 SIMILARITY:
                                                                                                                                                                                                                                               SUBCELLULAR SIMILARITY:
                                                                                                                                                                                                                                                                      PATHWAY: Lipoproteins biosynthesis. SUBCELLULAR LOCATION: Integral members.
                                                                                                                                                                                                                                                                                                                                              FUNCTION: Transfers the fatty acyl group
                                                                                                                                                                                                                                                                                                                                                                            Res.
                                                                                                                                                                                                                                                                                                                         (By similarity)
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214
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H3; 1.
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Pred. No. 19;
2; Mismatches
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LOMENAL (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
SH3.
                                                                                                                                                                                                                                          gral membrane protein (By similarity)
apolipoprotein N-acyltransferase
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                                                                                                                                              It is produced through a collaboration
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                        products.";
DNA Seq. 1::
-!- FUNCTION
                                                                                                             EMBL; X13536; CAA31887.1; HSSP; P02833; 9ANT.
                               Pfam; PF00046; homeobox; Pfam; PF04617; Hox9_act;
                                                              InterPro; IPR006711;
InterPro; IPR000047;
                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                PRINTS; PR00024; HOMEOBOX
                                                                                               InterPro;
                                                                                                                                                                                                                                                                                             <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                              Rubin M.R., Nguyen-Huu M.C.;
"Alternatively spliced Hox-1.7 transcripts encode different protein
                                                                                                                                                                                                                                                                                                                                                                                                                      Rubin M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p51783;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homeobox protein Hox-A9 (Hox-1.7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HXA9
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92190539; PubMed=1983703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Acyltransferase; TRANSMEM 6 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAMS; TIGR0054
PROSITE; PS50263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004563; Lnt.
InterPro; IPR003010; Ntlse/CNhydtse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                              Seq. 1:115-124(1990).

FUNCTION: Sequence-specific transcription factor which is part a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.

SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the Abd-B homeobox family.
                                              PF00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 GTASWCGLETLWSHSILWWSPV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; D90911; BAA18131.1; -. S75570; S75570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00795; CN_hydrolase; 1.
PR00031; HTHREPRESSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRASWC----WALALLWLAVV 26
                                                                                             IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 AA;
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47
83
126
174
206
277
496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; lnt; 1.
CN_HYDROLASE;
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146
194
226
297
516
519
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                                                            Hox9_act.
HTH_lambrepressr.
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67
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POTENTIAL.
POTENTIAL.
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HYDROLASE.
A28C75F260EF8BA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 AA
                                                                                                                                                                      (See http://www.isb-sib.ch/announce,
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,
Scheetz T.E.,
RA Diatchenko L., Marusina K., Farmer A.R., Rubin G.M., Hong L.,
Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Wolfernan K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McEernan K.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Schmutz J., Myers R.M.,
ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
ROdriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Grene E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDFL
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9HCN8; Q9BRI5;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Stromal cell-derived factor 2-like protein 1 precursor (SDF2 like protein 1) (PWP1-interacting protein 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "hPWP1-interacting p
Submitted (JUN-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21092619; PubMed=11162531; Fukuda S., Sunii M., Masuda Y., Takahashi M., Koike N., Teishima J., Yasumoto H., Itamoto T., Asahara T., Dohi K., Kamiya K.; Yasumoto H., Itamoto I. an endoplasmic reticulum stress-inducible gene and encodes a new member of the Pmt/rt protein family."; Biochem. Biophys. Res. Commun. 280:407-414(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDF2L1
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NON_TER 1 1
DNA_BIND 96 155
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PROSITE; PS50071; HOMEOBOX 2; 1.

Homeobox; DNA-binding; Developmental protein; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000010; Homeobox; SMART; SM00389; HOX; 1.
SUBCELLULAR LOCATION: Endoplasmic reticulum lumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSSRSRSSWCCNLKQLAFAGLAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein 8.";
0) to the EMBL/GenBank/DDBJ databases.
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43.5%;
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Pred. No. 14;
4; Mismatches
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; B84FA507EC67CF91 CRC64;
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5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 162;
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  (Potential)
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UCEFFEED BOSOSSPICKERATION
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                                                                                                                                                                                                                                                                                                                                                                      ESULT
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Best Local S
Matches 11
SEQUENCE FROM N.A.
STRAIN-C58 / ATCC 33970;
MEDLINE=21608550; PubMed=11743193;
MEDLINE=21608550; PubMed=11743193;
Mood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Riseida N.F. Jr., Woo L
Chura V.K., Zhou Y., Chen L., Mood G.E., Almedda N.F. Jr., Woo L
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Mu Z., Romero P., Gordo
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan
                                                                                                                                                                                                                                            PIC1 AGRT5 STANDARD; PRT; 233 AA. P29112; (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 24.9 kDa protein in picA locus (ORFI). ATU3128 OR AGR L 3363.
                                                                                                                                                                                                                                                                                                                                                       LT 13
_AGRT5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
                                                                                                                                                                           Rhizobiaceae; Rhizobium/Agrobacterium group; ROBI_TaxID=176299, 358;
                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                       Agrobacterium tumefaciens (strain C58 / ATCC 33970), and Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00014; ER TARGET; 1.
PROSITE; PS50919; MIR; 3.
Endoplasmic reticulum; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000886; E
InterPro; IPR003608; W
Pfam; PF02815; MIR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 607551;
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SIMILARITY: Contains 3 MIR domains.
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BC006248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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PROTEIN 1.
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MIR 2.
MIR 3.
PREVENT SECRETION FF
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L -> F (IN REF. 2 AN
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Pred. No.
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2 AND 3).
EF CRC64;
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    Perry M.,
Dolan M.,
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RESULT 14
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P10493;
 SEQUENCE
                                                                                    Nidogen precursor
NID OR NID1 OR ENT
                                                                                                                01-APR-1990 (Rel.
01-APR-1990 (Rel.
15-MAR-2004 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rong L., Karcher S.J., Gelvin S.B.;

"Genetic and molecular analyses of picA, a plant-inducible locus on the Agrobacterium tumefaciens chromosome.";

J. Bacteriol. 173:5110-5120(1991)

-i- FUNCTION: SEEM TO REGULARIES THE SURFACE PROPERTIES OF THE BACTERIUM IN THE PRESENCE OF PLANT CELLS OR PLANT CELL EXTRACTS.

MUTATIONS IN THIS PROTEIN ARE RESPONSIBLE FOR AN INCREASED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C58 / ATCC 33970;
MEDLINE=21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Cielo C., Slater S.;
                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE009243; AAL43944.1; ALT_INIT.
EMBL; AE008370; AAK90258.1; ALT_INIT.
EMBL; M62814; AAA22103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chumley F., Tingey S.V., Nester E.W.;
"The genome of the natura
                       NCBI_TaxID=10090;
                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58."; Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 294:2317-2323(2001)
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDUCTION: By certain acidic polysaccharides found in carrot root extract. This induction may be regulated by the polygalacturonase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGREGATION OF THE BACTERIA IN THE
                                                                                                                                                                                                                                                                                                                                                                                                   B40364; B40364.
                                                                                                                                                                            MOUSE
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FROM N.A.,
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                                                                                                                                                                                                                                                                               RRGAGAARGRASWCWALALLWLAV 25
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                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                           STANDARD;
                                                                                                                  14,
                                                                                                    (Entactin).
                                                                                                                                                                                                                                                                                                                                                                       24935 MW;
 AND
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                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                              Created)
 SEQUENCE
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                                                                                                                                                                                                                                                                                                                            Score 48;
Pred. No.
                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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 OF.
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J. Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97446166; PubMed=9299350;
Adam S., Goehring W., Wiedemann H., Chu M.-L., Timpl R., Kostka G.;
"Binding of fibulin-1 to nidogen depends on its C-terminal globular
domain and a specific array of calcium-binding epidermal growth
factor-like (EG) modules.";
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21474010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matrix 13:215-222(1993).
[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93316903; PubMed=8326911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Exon organization of the mouse entactin gene corresponds to the structural domains of the polypeptide and has regional homology to the low-density lipoprotein receptor gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1207-1245 FROM N.A. STRAIN-C57BL/6J X CBA/J; MEDLINE=95224912; PubMed=7601446; Durkin M.E., Wewer U.M., Chung A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene
                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH FBLN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujiwara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragmented nidogen obtained from a tumor basement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Purification and structural characterization of intact and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paulsson M., Deutzmann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 26:219-228(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94040771; PubMed=8224873; Durkin M.E., Liu S.H., Reing J., Chung "Characterization of the 5' end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO
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Yamamda Y., Pan T.-C., Conway D., Chu M.-L.;
"Amino acid sequence of mouse nidogen, a multidomain basement
membrane protein with binding activity for laminin, collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sujiwara S., Shinkai H., Mann K., Timg
Structure and localization of O- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             basement membrane protein, entactin.";
Gene 132:261-266(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c;
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receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89079780; PubMed=3264556;
Durkin M.E., Chakravarti S., Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTERACTION WITH FBLN1.
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SIMILARITY: Contains 6 EGF-like domains.
SIMILARITY: Contains 1 thyroglobulin type-I domain.
SIMILARITY: Contains 5 LDL-receptor YWTD domains.
                                                                    SUBUNIT: Interacts with FBLN1.
SUBCELLULAR LOCATION: Basement membranes.
PTM: N- and O-glycosylated.
                                                                                                                                                                                                         FUNCTION: Sulfated glycoprotein which is widely distributed in basement membranes and that is tightly associated with laminin.
                                                                                                                                                       Also binds to collagen IV. It probably has extracellular matrix interactions.
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N-linked oligosaccharide chains
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Pfam; PF00008; EGF; 6.

Pfam; PF00058; 1dl recept b; 3.

Pfam; PF00086; thyroglobulin_1; 1.

SMART; SM00179; EGF_CA; 2.

SMART; SM00182; G2F; 1.

SMART; SM00135; LY; 5.

SMART; SM00131; TY; 1.

SMART; SM00211; TY; 1.
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EMBL; X14480; CAA32642.1; -.
EMBL; L17324; AAA77652.1; JOINED.
EMBL; L17323; AAA77652.1; JOINED.
EMBL; L17323; AAA77652.1; JOINED.
EMBL; K17323; AAA77652.1; JOINED.
EMBL; X63093; CAA58148.1; -.
PIR; S02730; MYMSND.
PDB; 1614; 28-NOV-01.
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30; GO:0005604; C:basement membrane; IDA.
30; GO:0005515; F:protein binding; IPI.
30; GO:0007160; P:cell-matrix adhesion; IDA.
30; GO:0007160; P:cell-matrix adhesion; IDA.
30; GO:0007160; P:cell-matrix adhesion; IDA.
31nterPro; IPR000152; Asx hydroxyl_S.
32interPro; IPR0001881; EGF_Ca.
32interPro; IPR006209; EGF like.
33interPro; IPR0003017; GFF_like.
33interPro; IPR000318; Gff_rike.
33interPro; IPR000318; Midogen_ext.
33interPro; IPR0003186; Nidogen_ext.
33interPro; IPR000316; Thyroglobulin_1.
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EGF_1; 1.
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; Extracellular matrix; Glycoprotein; Sulfation; inding; Repeat; EGF-like domain; Cell adhesion;
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EMBL; U14003; AAA97166.1; ALT_INIT.
EMBL; AE000497; AAC77226.1; ALT_INIT
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                                                                                                                                                                                                                                                                                  MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
Blatther F.R.,
"Analysis of the Escherichia coli genome VI: DNA sequence of the
region from 92.8 through 100 minutes.",
Nucleic Acids Res. 23:2105-2119(1995).
-!- COPACTOR: Binds 2 zinc ions per subunit (By similarity).
-!- COPACTOR: Binds 2 zinc ions per subunit alcohol dehydrogenase
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P27250; P76812;
P1-AUG-1992 (Rel. 23, Created)
01-FBS-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical zinc-type alcohol dehydrogenase-like protein yjgB.
YJGB OR B4269.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

»sult No.	Score	Query Match	Length	DB	ID	Description
1	66	42.9	909	17	Q9HMT4	Q9hmt4 halobacter:
Ŋ	59	38.3	412	16	Q92VB2	•••
ω	59	38.3	588	16	Q82G94	_
4	58	37.7	146	드	Q8CEK6	٠,
v	57.5	37.3	343	16	Q8G419	Ψ.
9	57	37.0	366	10	Q84X72	N
7	56	36.4	214	16	069464	
œ	56	36.4	485	16	Q88SV3	
9	55.5	36.0	412	10	Q7XSY0	
10	55.5	36.0	695	16	Q8XWW4	Q8xww4 ralstonia s
11	ភភ	35.7	147	10	Q7X917	
12	55	35.7	304	16	Q7WFK8	Q7wfk8 bordetella
13	ប	35.7	304	16	Q7W451	Q7w451 bordetella
14	55	35.7	707	10	Q9ZRA6	Q9zra6 chlamydomon
15	55	35.7	3019	12	092529	
16	54.5	35.4	205	16	Q8PDF8	Q8pdf8 xanthomonas

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Q8h053 oryza sativ		Q92ui9 rhizobium m	xanth	shige		oryza	Q90584 gallus gall	oryza	-	homo		Q9bx78 homo sapien		Q7xtz2 oryza sativ	a			Q8ud14 agrobacteri		Q82hw2 streptomyce		lcaligene	Q81311 vitreoscill	xylella	xylella	Q9xeq6 sorghum bic	bradyrhi	Q9xe69 sorghum bic

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Q92VB2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical membrane protein SMD21292.
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Q82G94;
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InterPro; IPR000847; HTH_Lysr.
Pfam; PF00528; BPD transp; 2.
PROSITE; PS00404; BPD TRANSP INN MEMBR; 1.
PROSITE; PS00044; HTH_LYSR FAMILY; 1.
Transmembrane; Transport; Complete proteome.
SEQUENCE 606 AA; 63066 MW; 2E64B9A20298A28C CRC64;
                                                                                            Hypothetical SAV4004.
                                                                                                                                         01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
Streptomycineae; Streptomycetaceae; Streptomyces NCBI_TaxID=33903;
                                                                   Streptomyces avermitilis.
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Rhizobium meliloti (Sinorhizobium meliloti)
                                            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0046821; C:extrachromosomal DNA; IEA.
GO; GO:0005489; F:electron transporter active
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000345; Cytc heme BS.
PROSITE; PS00199; CYTOCHROME C; 1.
Plasmid; Hypothetical protein; Complete protein active for the protein 
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Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
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6; Mismatches
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MEDLINE=21477403; PubMed=11572948;
Omura S., Tkeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: deducing the ability of producing secondary
metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                        The FANTOM Consortium,
the RIKEN Genome Exploration Research
"Analysis of the mouse transcriptome k
60,770 full-length CDNAs.";
Nature 4200:563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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STRAIN=C57BL/6J; TISSUE=Diencephalon;
MEDLINE=22354683; PubMed=12466851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein (Fragment). 9330132005RIK.
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01-JUN-2003
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Sakaki Y., Hattori M., Omura S.;
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MEDLINE=22608306; PubMed=12692562;
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SEQUENCE FROM N.A.
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(TrEMBLrel. 24, Last annotation update)
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3428 MW; D8DC5F23BE49A321 CRC64;
                                                                                                                                   Score 58; DB Pred. No. 3.7; 1; Mismatches
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Pred. No. 9
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Q84X72;
Q94X72;
Q1-JUN-2003 (TrEMBLrel. 24, Created)
Q1-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CR066 protein.
Chlamydomonas reinhardtii.
Chlamydomonas Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
 ML1666 O
                                                                                                                                                                                                                                                                                                                  "Finished genomic sequence in Chlamydomonas."; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ EMBL; AY207499; AAO32622.1; -.
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Li J.B., Lin S., Jia H.,
                         Putative integral membrane
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Dutcher S.K.;
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Bifidobacteriaceae; Bifid
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2; Mismatches
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Matches 7
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Best Local Similarity
                                                                                                                                                                                                                                    "Complete genome sequence of Lactobacillus plantarum WCFS1.", Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
EMBL; AL935261; CAD65406.1; -.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                   Pfam, PF00614; PLDc; 2.
PROSITE; PSS0035; PLD; 2.
Transferase; Complete proteome.
SEQUENCE 485 AA; 55778 MW;
                                                                                                                                                                                                                                                                                                                                                                   Kleerebezem M., Boekhorst J., van Kranenburg R., M
Kuipers O.P., Leer R., Tarchini R., Peters S.A., S
Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M.,
Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De V
De Vos W.M., Siezen R.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-NCIMB 8826 / WCFS1;
MEDLINE=22480296; PubMed=12566566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLS OR LP 3273.
Lactobacillus plantarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL023635; CAA1918B.1; -.
EMBL; AL583923; CAC30619.1; -.
PIR; T44701; T44701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cardiolipin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q88SV3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Squares S., S
Barrell B.G.;
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NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leproma; ML1666; -.
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  Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGAGAARGRASWCWALALLWLAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TIEMBLrel. 24, Created)
(TIEMBLrel. 24, Last sequence update)
(TIEMBLrel. 25, Last amoutation update)
synthetase 2 (EC 2.7.8.-).
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                      36.4%;
46.7%;
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41.7%;
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••
Score 56; DB
Pred. No. 20;
4; Mismatches
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Pred. No. 9.5;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                        C725C28841DF8D31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5B48414709828FA0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 485
                DB
20;
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9.5;
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                                                 16;
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                                                 Length 485;
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Sandbrink H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Bron P.A.,
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ASWCWALALLWLAVV

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P. SEQUENCE FROM N.A.

A Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,

A Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,

A Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,

Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,

A Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,

A Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,

A Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,

A Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,

A Chang R.Q., Guan J.P., Hong G.F.,

L Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AL606602; CAE01753.1; -.

SEQUENCE 412 AA, 45803 MW, 1A8FE5323333606C8 CRC64;
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おどばばばいらじじを対するなるなんなんにある。
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Best Local S
Matches 11
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin M., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; "Butre 415:497-502(2002).

Bature 415:497-502(2002).

EMBL, AL646059; CAD16083.1; -.

GO; GO:0001658; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0004851; F:uroporphyrin-III C-methyltransferase activity; I
                                                                                                                                                                                                               STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                           QBXWW4;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable bifunctional: uroporphyrin-III C-methyltransferase
uroporphyrinogen-III synthase transmembrane protein
(EC 2.1.1.107).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7XSY0;
01-0CT-2003
01-0CT-2003
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                                                                                                  Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                         RSC2356 OR RS01190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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01-0CT-2003 (TrEMBLrel.
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40.7%;
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Last annotation update)
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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     activity; IEA.
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RESULT 12 Q7WFK8

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Q7WFK8;

PRELIMINARY;

PRT;

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Q7X917
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                                                                       Query Match
Best Local S
Matches 9
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Best Local
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EMBL, AL662965; CAD39623.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
Gub J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004852; F:uroporphyrinogen-III synthase activity; GO; GO:006783; P:heme biosynthesis; IEA.
InterPro; IPR007470; DUFS13.
InterPro; IPR003754; HEM4_Synth.
Pfam; PF02602; HEM4; 1.
Pfam; PF02602; HEM4; 1.
Pfam; PF04375; HemX; 1.
Transferase; Methyltransferase; Complete proteome.
SEQUENCE 695 AA; 73670 MW; 1649C5BA781DF0F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update
CSJNBa0040D17.2 protein (OSJNBb0033G08.19 protein)
OSJNBA0040D17.2 OR OSJNBB0033G08.19.
Oryza sativa (Rice)
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Q7X917;
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                                                                       Similarity 9; Conser
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RRACGSSRERDGWAWHSCVAMAQITPG 125
                                RRGAGAARGRASWCWALALLWLAVVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
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                                                                                                                                            147 AA;
                                                                       Conservative
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                                                                                                                                            14767 MW;
                                                                                    35.7%;
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Pred. No. 32;
1; Mismatches
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                                                                   Score 55; DB 10; Length 147; Pred. No. 9.2; Mismatches 14; Indels
                                                                                                                                            024314375754B785 CRC64;
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SEQUENCE FROM N.A.

SITRAIN=12822 / AICC BAA-587;

SITRAIN=12822 / AICC BAA-587;

KMEDILINEE22827954; PubMed=12910271;

Rarkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

Harris D.E., Holden M.T.G., Churcher C. M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Peltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Weil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

Nat. Genet. 35:32-40 (2003).

REBL; Bx640434; CAE39102.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3SULT 13
7W451
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Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
A Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
Unwin L., Whitehead S., Barrell B.G., Waskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella paraperussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
EMBL, B&40450; CAB34627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local (
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01-OCT-2003 (Tremblrel. 25,
01-OCT-2003 (Tremblrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alcaligenaceae; Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bordetella parapertussis.
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01-OCT-2003
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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01-OCT-2003 (TremBLrel.
01-OCT-2003 (TremBLrel.
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NCBI_TaxID=518;
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304 AA;
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31640 MW;
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Last annotation update)
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Pred. No.
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7AF46DA2FB95EFC0 CRC64
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RESULT 15
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genetic groups.";
J. Gen. Virol. 79:1847-1857(1998).
-!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1998 (TrEMBLrel. 08, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U77388; AAD00267.1; -.
GO; GO:0003871; F:5-methyltetrahydropteroyltriglutamate-homoc.
GO; GO:0009986; P:methionine biosynthesis; IEA.
                                                                                                                                                Tokita H.,
Mayumi M.;
                                                                                                                                                                                    MEDLINE=98378034; PubMed=9714232;
                                                                                                                                                                                                                                                                                                              Okamoto H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome polyprotein.
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002629; Methionine synth.
Pfam; PF01717; Methionine synt; 1.
ProDom; PD004692; Methionine synt; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henskens H., den Hartog M.;
"A methionine synthase.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas moewusii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                             "The entire nucleotide sequences of three in genetic groups 7-9 and comparison with
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Submitted (MAR-1996)
                                                                                                                                                                                                                                                                                                                                 STRAIN=Th580;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                            Hepacivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses,
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                                                                                                                                                                   H., Iizuka H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.7%;
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Pred. No. 18;
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Pred. No. 38;
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M InterPro; IPRO09003; Cys Ser trypsin.

M InterPro; IPRO0252; HCV_capsid.

M InterPro; IPRO0252; HCV_capsid.

M InterPro; IPRO0252; HCV_capsid.

M InterPro; IPRO0253; HCV_NS1.

M InterPro; IPRO0253; HCV_NS1.

M InterPro; IPRO0253; HCV_NS4.

M InterPro; IPRO0253; HCV_NS4.

M InterPro; IPRO0253; HCV_NS4.

M InterPro; IPRO0149; HCV_NS4A.

M InterPro; IPRO0149; HCV_NS4A.

M InterPro; IPRO01650; HelTcase_C.

M InterPro; IPRO01650; HCV_NS5A.

M InterPro; IPRO0106; HCV_RdRP.

M InterPro; IPRO0109; RNA_pol_DS_PS

M InterPro; IPRO0109; RNA_pol_DS_PS

M InterPro; IPRO07094; RNA_pol_PSVIr.

M Pfam; PP01543; HCV_capsid; 1.

M Pfam; PP01542; HCV_NS1; 1.

M Pfam; PP01542; HCV_NS2; 1.

M Pfam; PP01560; HCV_NS3; 1.

M Pfam; PP01560; HCV_NS3; 1.

M Pfam; PP01560; HCV_NS4; 1.

M Pfam; PP01006; HCV_NS4; 1.

M Pfam; PP01006; HCV_NS4; 1.

M Pfam; PP01006; HCV_NS4; 1.

M Pfam; PP010071; helTcase_C; 1.

M Pfam; PP010071; helTcase_C; 1.

M Pfam; PP01098; Viral RdR; 1.

M Pfam; PP01098; Viral RdR; 1.

M Pfam; PP01098; Viral RdR; 1.

M Pfam; PP0100; IDENDC; 1.

M Pfam; PP0100; IDENDC; 1.

M Pfam; PP0100; INPOLOSE;                                                                                                                                                                                                                                                                                                                                                                                                   learch completed: June 8, 2004, 14:07:06
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REMBL; D84262; BAA32664.1; -.

RESSP; P27958; JAIV.

MEROPS; U39.001; -.

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Best Local S
Matches 9
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                                                                                                                                   AASAAGTAGWCWTLIFL 777
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52.9%;
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Pred. No. 1.4e+02;
Pred. No. 7;
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length: 2000000000
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geneseqp2004s:*
               geneseqp2003as:*
geneseqp2003bs:*
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geneseqp2001s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	o.	ຫ	4	w	2	ᅩ	esult No.
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Ruben & Wei Y, Shi Y,

SM, Ni J, Ro C, Endress GA, C, Moore PA;

Rosen CA, Y A, Duan RD,

Yu G, Young PE, Feng F, Soppet DR; , Kyaw H, Ebner R, Lafleur DW, Olsen HS;

WPI; 1999-562050/47. N-PSDB; AAZ24826.

45	44	43	42	41	40	39	38	37	36	S	ω 4.	ω ω	32	31	30	29	28	27	26
52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	52.5	53	53	53	. 53	53	53
31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.1	31.4	31.4	31.4	31.4	31.4	31.4
575	575	575	551	442	360	341	333	267	244	206	199	199	199	600	532	346	243	243	211
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AAR76500	AAP90547	AAP70195	AAR76503	AAP90475	ABU22472	AAY69880	AAG91017	AAB79568	AAM42195	AAB42500	ADE09108	ADE09107	AAU28370	ABG07764	AAY84593	ABG96249	ABM43008	AAU46489	ABG01709
Aar76500	Aap90547	Aap70195	Aar76503	Aap90475	Abu22472	Aay69880	Aag91017	Aab79568	Aam42195	Aab42500	Ade09108	Ade09107	Aau28370	Abg07764	Aay84593	Abg96249	Abm43008	Aau46489	Abg01709
Cattle MI	Bovine Mu	Sequence	Cattle MI	N-termina	Protein e	B. lactof	C glutami	Corynebac	Human pol	_	Novel pro	Novel pro	Novel hum			Maize per	Propionib	Propionib	Novel hum

ALIGNMENTS

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RESULT 1
AAY41323
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19-MAR-1998
                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blod; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                   WO9947540-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein encoded by gene 16 clone HMZAD77.
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                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                    18-MAR-1999;
                                                                                                                                                                                                                                                                                            23-SEP-1999.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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98US-0078581P.
98US-0080312P.
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98US-0080313P.
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98US-0078577P.
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98US-0078574P.
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AM93870
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Best Local :
                                                                                                                                                                                                                                                  WPI; 200
N-PSDB;
The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful
                                                                                                                                                                                                     830
                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUL-1999; 99JP-00194486.
11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; full length cDNA; cDNA synthesis; oligo-capping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human polypeptide, SEQ ID NO: 3978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a secreted human protein encoded by the gene clone detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin rc portion (e.g. AAZZ4802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences: AAZZ4811-2Z2907; amiro acid sequences AAY410308-Y41040) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Alsc, pathological conditions can be diagnosed by determining the amount of the
                                                                                                                              Claim 8;
                                                                                                                                                                                                                                                                                                                         Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001
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                                                                                                                                                                                             Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (see AAZ24811 for described uses)
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)B; AAK94829.
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                                                                                                                      SEQ ID NO 3978; 1380pp + Sequence Listing;
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                                                                                                                                                                           manipulation
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                                                                                                                                                                                                                                                                                                                      Sugiyama
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K, Kojima
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T, Koga
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Best Local S
Matches 30
This invention describes the isolation of a novel human secreted protein, zsig46 encoded by a gene on chromosome 13 which is mainly expressed in the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zsig46, which may be associated with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschaprung's disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger syndrome). Antibodies and other binding proteins, are used as immunoassay reagents to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity purification of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radioisotopes etc. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secreted protein; zsig46; human; chromosome 13; thyroid; hypothyroidism; Graves disease; thyrotoxicoxis; thyroid Hirschsprung's disease; neuronal ceroid-lipofucinosis; W Reiger syndrome; immunoassay; detection; anti-idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New secreted polypeptide, zsig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases involving genes on chromosome
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Pred. No. 9e-15;
Mismatches
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differentiation and proliferation of specific cell eating (extra)thyroid diseases or as additive to ce

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Sequences AAU29380-AAU29509 represent human G protein-coupled receptor (GPCR) polypeptides of the invention. The proteins and the DNA sequences encoding them can be used to identify compounds which bind to GPCR polypeptides and in screening for compounds that modulate GPCR activity. By screening a human subject for the presence of mutations in GPCR DNA, GPCR-related disorder or a genetic predisposition can be diagnosed. The sequences can also be used for treatment and prevention of mental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000;
16-MAR-2000;
16-MAR-2000;
16-MAR-2000;
                                                                                                                                                                   Claim 31;
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                                                                                                                                                                                                        prevention,
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29-MAR-2000;
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DB; AAS46857.
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No. 7.8e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis;
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RESULT 5
ABG60706
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                                                                                                                                                                                                                                                                                                      16-MAR-2000;
16-MAR-2000;
16-MAR-2000;
                                                New isolated nucleic acid encoding a G producing the receptor which can induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g protein coupled receptor; nGPCR-x; immune response; thyroid disorder;
mental disorder; thyreotoxicosis; myxcedema; inflammatory condition;
Crohn's disease; cell differentiation; homeostasis; rheumatoid arthritis;
renal failure; autoimmune disorder; movement disorder; CNS disorder;
                     Claim 27; Page 44; 216pp; English.
                                                                                     N-PSDB; ABK81635.
                                                                                                  WPI; 2002-434856/46.
                                                                                                                                                                                                                                                      24-MAR-2000;
27-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viral infection; human immunodeficiency virus; HIV; metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis, thyroid disorders such as myxoedema, neurodegenerative disorders such as Parkinson's disease, cardiovascular disorders such as atherosclerosis, renal failure, autoimmune disorders, hyperproliferative disorders such as psoriasis and viral infections such as those caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders such as schizophrenia, neurological disorders such depression, metabolic disorders such as obesity, cancer, rheu arthritis, thyroid disorders such as myxoedema, neurodegenera disorders such as Parkinson's disease, cardiovascular disorder
                                                                                                                                                  (VOGE/) VOGELI G.
                                                                                                                                                                            29-MAR-2000;
                                                                                                                                                                                                  29-MAR-2000;
                                                                                                                                                                                                                 29-MAR-2000;
                                                                                                                                                                                                                             29-MAR-2000;
29-MAR-2000;
                                                                                                                                                                                                                                                                                16-MAR-2000;
                                                                                                                                                                                                                                                                                            16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                         16-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         porliferative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular disorder; diabetes; obesity; anorexia; cardiomyopathy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              dysfunction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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2000US-019155P.
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2000US-0192830P.
2000US-0192916P.
2000US-019293P.
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                                                                                                                                                                            2000US-0192945P
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2000US-0189918P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coupled receptor
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Pred. No. 2.7;
2; Mismatches
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                                                          protein coupled receptor
                                                an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lung cancer; hormonal
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                                              in a mammal.
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The invention describes an isolated

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosie; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anorexia, cardiomyopathies), porliferative diseases and cancers (e.g., psoriasis, lung cancer), hormonal disorders, sexual dysfunction and hereditary mental disorders in a human patient. A host cell comprising (I) is used to screen for a modulator of nGPCR-x activity, nGPCR-x is used to identify compounds that can treat mental disorders. The polypeptide encoded by (I) is used to purify a G protein from a sample. This is the amino acid sequence of a novel G protein coupled receptor (nGPCR-x) protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thyreotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g. Crohn's disease), diseases related to cell differentiation and homeostasis, rhematoid arthritis, autoimmune disorders, movement disorders, CNS disorders, viral infections (e.g. Human immunodeficiency virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity, virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity,                                        Example 4; Page 543-544; 894pp; English
                                                                                                                                            Isolated polypeptides useful f
nervous system disorders, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-2000; 2000US-00491404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human novel protein #33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    predisposition disorder, such as a mental disorder. (I) is used to screen for an nGPCR-x related disorder including thyroid disorders (e.g. thyreotoxicosis. myxoedema), renal failure, inflammatory conditions (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence encoding a portion of a G protein coupled receptor (nGPCR-x).

(I) is used to produce a recombinant nGPRC-x polypeptide. A polypeptide encoded by (I) is used to induce an immune response in a mammal. nGPRC-y is used to identify a compound that binds to it and/or modulates it's activity. (I) is used to identify animal homologues of nGPCR-x. (I) can be used to diagnose a human subject as having a brain or genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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DB; AAS22467.
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ll; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                      for treating anti-inflammatory diseases, d for regenerating bone and cartilage.
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies craised against the polypeptides are used in a method of treatment of a CC mammal and prevention of disorders caused by the aberrant protein CC expression or activity. The polypeptides can be used as molecular weight expression or activity. The polypeptides can be used as molecular weight care used to identify compounds which bind to the polypeptides. CC Polynucleotides of the invention are used as probes and primers, for crecombinate proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a cumour, in assays to determine biological activity, to raise cantibodies/elicit an immune response, to determine quantitative protein clevels, as tissue markers, and to isolate receptors or ligands. CC Polypeptides of the invention may also be useful in treating platelet cd isorders, stem cell disorders, regenerating bone, cartilage, tendon, cligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, cc allamer's, Parkinson's and Mintington's diseases, amylotrophic lateral contends of the invention or from autoimmunity, cancer, allergy, asthma, graft-currous system disorders, and infection. The present sequence cc represents a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 14
                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                  N-PSDB; AAS93439.
                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #29243
                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                          11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; food supplement; medical in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG29252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG29252 standard;
                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-2002
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                                                                                                                   2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 RGEGETWGRVTMTKLAQWLWGLAILGSTWVALTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 RGAGAARGR----ASWCWALALL---WLAVVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                   HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                           imaging;
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                                                                                                                                                                                                                                                                                                                                                                                                         gene mapping; gene therapy; forensic
maging; diagnostic; genetic disorder.
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Pred. No. 2.4;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           torensic;
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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene therapy; vaccine; lung specific antigen; cancer diagnosis; cancer monitoring; cancer staging; cancer imaging; lung cancer; non-cancerous diseases of the lung; transgenic animal.
The invention describes an isolated human nucleic acid (I) of 120 10-1533 residue amino acid sequences (S1), given in
                                                                                              Claim 11; Page 359-360; 389pp; English.
                                                                                                                                                           New isolated human nucleic acid molecule and polypeptide, useful for identifying, diagnosing, monitoring, staging, imaging and treating cancer and non-cancerous diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                  WPI; 2002-713376/77.
                                                                                                                                                                                                                                                                                                                                                              Macina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-2000; 2000US-0252500P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-NOV-2001; 2001WO-US043612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC
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                              encoding any
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                                                                                             The invention relates to avilamycin derivatives (I) with antibacterial, virucide, protozoacide and fungicide activity. (I) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aureus. (I) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin A biosynthetic gene cluster (ABZ37515-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification, comprising any of 164 179-12421 base pair sequences (S2), given in the specification. The methods and compositions of the present invention are useful for identifying, diagnosing, monitoring, staging, imaging and treating lung cancer and non-cancerous diseases of the lung. They are also used for identifying lung tissue, monitoring and identifying and/or designing antagonists of the polypeptide of the invention, gene therapy, production of transgenic animals and production of engineered lung tissue for treatment and research. This is the amino acid sequence of a lung specific nucleic acid
                                                                                                                                                                                                                                                                  New avilamycin derivatives, useful for treatment of infections, nucleic acid encoding avilamycin synthesis enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **vilamycin; antibacterial; virucide; protozoacide; fungicide; infection; medicine; Staphylococcus aureus; biosynthetic gene cluster; enzyme.
                                                    Sequence 19938 AA;
                                                                                                                                                                                                                                                                                                                      N-PSDB; ABZ37516.
                                                                                                                                                                                                                                                                                                                                      WPI; 2003-018650/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces viridochromogenes Avi gene cluster polypeptide frame 6.
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                                                                                                                                                                                                                                   Example 1; Page 68-301; 319pp; German
                                                                                                                                                                                                                                                                                                                                                                     Weitnauer G,
                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2001; 2001DE-01009166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-2001; 2001WO-EP009815
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                                                                                     ABZ37516)
                                                                                                                                                                                                                                                                                                                                                                                                      (COMB-) COMBINATURE BIOPHARM AG.
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12; Conserv
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34.0%;
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Score 57.5;
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Pred. No. 5.8;
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5; DB 6;
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               Length 19938;
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                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a novel method for identifying essential genes for survival or virulence of mycobacteria species. The method comprises aligning the genomic sequence of a first mycobacterium species on a genomic sequence of a second mycobacterium species and selecting a polynucleotide sequence that is highly conserved in both genomes with no counterparts in other bacterial genomic sequences and that corresponds to an essential gene for the survival or virulence of mycobacterium species. The method of the invention is useful for detecting M. tuberculosis or M. leprae infection. The method reduces the number of potential new targets and prevent mycobacterial diseases, particularly tuberculosis and leprosy. The present sequence represents a marker protein from Mycobacterium tuberculosis and Mycobacterium leprae identified using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying and selecting genes for survival or virulence of mycobacteria by a comparative genomic analysis of the sequences of Mycobacterium tuberculosis and M. leprae.
                      20-MAY-2003
                                                        ABU65190;
                                                                                    ABU65190 standard; protein;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 376-377; 874pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M. tuberculosis and M. leprae marker
                                                                                                                                                                                                                                                                                                                                                                  method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-759885/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU05547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-2001; 2001US-0270123P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2002; 2002WO-IB001973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU05547 standard; protein; 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INSP ) INST PASTEUR.
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                                                                                                                                                                                 175 RTSAIARGIYOWRWSIATLWFITV 198
                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                   RGAGAARGRASWCWALALLWLAVV 26
                                                                                                                                                                                                                                                                                                                              214 AA;
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                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                    (first entry)
                                                                                                                                                                                                                                                                     33.1%;
41.7%;
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 10-JUL-2001
31-JUL-2001
16-AUG-2001
10-SEP-2001
11-SEP-2001
27-SEP-2001
27-SEP-2001
27-SEP-2001
31-CCT-2001
31-CCT-2001
14-NOV-2001
                                                                                                                                                                                                                                                                                                                        02-MAY-2001;
03-MAY-2001;
03-MAY-2001;
15-MAY-2001;
16-MAY-2001;
16-MAY-2001;
31-MAY-2001;
31-MAY-2001;
18-JUN-2001;
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26-MAR-2001;
27-MAR-2001;
27-MAR-2001;
28-MAR-2001;
30-MAR-2001;
30-MAR-2001;
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20-MAR-2001;
20-MAR-2001;
20-MAR-2001;
21-MAR-2001;
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13-APR-2001;
30-APR-2001;
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08-MAR-2001;
08-MAR-2001;
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19-JUN-2001;
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02-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001US-0278152P.

2001US-0278894P.

2001US-0278999P.

2001US-0279036P.

2001US-0279344P.

2001US-0277338P.

2001US-0277935P.

2001US-0280833P.

2001US-0280832P.
2001US-0332271P.
2001US-0332272P.
2001US-0333184P.
2001US-0333272P.
2001US-0332094P.
2001US-0337426P.
                                                                                                     2001US-0280822P

2001US-0280900P

2001US-0281194P

2001US-0283675P

2001US-0288066P

2001US-0288066P

2001US-0291199P

2001US-0291290P

2001US-0291240P

2001US-0291240P

2001US-0294899P

2001US-0294899P

2001US-0294899P

2001US-0294899P

2001US-0294899P

2001US-0294899P

2001US-0294899P

2001US-039303P

2001US-0318462P

2001US-031870P

2001US-0325430P

2001US-0325430P

2001US-0325681P

2001US-0335301P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 2001US-0276000P.
; 2001US-0276776P.
; 2001US-0276994P.
; 2001US-0277239P.
; 2001US-0277321P.
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2001US-0277833P.
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2001US-0274849P,
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2001US-0275601P
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2001US-0275578P.
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ESULT 1:
AR41001
  Query Match
Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes novel human NOVX polypeptides which have cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensi activity. Pharmaceutical compositions comprising the NOVX proteins or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing or nucleic acid molecules or NOVA antibodies are useful for preventing the nucleic acid molecules or NOVA antibodies are useful for preventing the nucleic acid molecules or NOVA antibodies are useful for preventing the nucleic acid molecules are useful for preventing the nucleic acid molecules are n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CEA, Li L;
Zerhusen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
Patturajan M, Gangolli E, Vernet CAM, Guo X, Tchernev V;
Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
Spaderna SK, Catterton E, Burgess C, Leite M, Zhong H, Alsobrook JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-2001; 2001US-0338092P
04-DEC-2001; 2001US-0337185P
03-JAN-2002; 2002US-0345705P
07-MAR-2002; 2002US-00092900.
                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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20-FEB-1992;
                                                19-FEB-1993;
                                                                                                                                                      WO9317104-A1
                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                      polymerase
                                                                                                                                                                                                                                                                                                                                                                                                            Abnormality; muscular dystrophy; CHR 19; chromosome 19; protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR41001;
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                                                                                                                                                                                                                                                                                                                                   sapiens.
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DB; ABX97157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myotonic
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                                                                                                                                                                                                                                                                                                                                                                                    chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first en
92US-00839255
                                                                                                                                                                                                                                                                                                                                                                                                                                                               dystrophy gene protein.
                                                93WO-US001545
                                                                                                                                                                                                    /note= "encoded by predicted reading frame a,
sequence indicate stop codons in the reading
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                      reaction; brain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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RESULT 13
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Matches
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                            Claim 1; Page 246-248; 471pp; Japanese.
                                                       Human protein originated from tumor cell line, applicable as reagent for studying intracellular protein networks and protein drug screening, also encoded cDNA for gene diagnosis and
                                                                                                N-PSDB;
                                                                                                                             Kato
                                                                                                                                                                    14-MAR-2000;
30-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence is that encoded by predicted reading frame a of the humyotonic dystrophy (DM) gene. It may be used in the identification individuals affected by DM. (Updated on 25-MAR-2003 to correct PN f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence of identify CHR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1993-288410/36.
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                                                therapy
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10-FEB-2000;
                                                                                                                                                                                                                                        06-DEC-1999;
06-DEC-1999;
                                                                                                                                                                                                                                                                      06-DEC-2000; 2000WO-JP008631
                                                                                                                                                                                                                                                                                         14-JUN-2001.
                                                                                                                                                                                                                                                                                                             WO200142302-A1
                                                                                                                                                                                                                                                                                                                                                                     Human protein HP03145
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG93279 standard; protein; 371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 6; 64pp; English.
                                                                                                                                                                                        14-FEB-2000;
                                                                                                                                                                                                 14-FEB-2000;
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Human; gene therapy; tumour
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                                                                                                                                                 (NISC-)
                                                                                                                                                                                                           10-FEB-2000;
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nes 15; Conserv
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                                                                                                          2001-381646/40.
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                                                                                                                                                 JAPAN SCI & TECHNOLOGY
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                                                                                                                            Eguchi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Housman DE;
                                                                                                                                                                   7, 2000JP-00031062.
7, 2000JP-00034090.
7, 2000JP-00035829.
7, 2000JP-00035829.
7, 2000JP-00071161.
7, 2000JP-00160851.
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                                                                                                                                                                                                                                                   99JP-00346863
                                                                                                                                                                                                                                        99JP-00346864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myotonic dystrophy gene - used to produce probes and abnormality and protein kinase reponsible.
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Pred. No.
                                                                                                                                                 CORP.
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67;
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                                                                    protein
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                                                               s drug,
tein source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the human
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The present sequence is a human protein. The human originated from tumour cell line, is applicable as

protein, preferably a drug, a reagent for

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RESULT 14
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Best Local
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12-JAN-2001;
12-JAN-2001;
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12-JAN-2001;
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                                                                                                                                                                                                                                                                                                          12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
12-JAN-2001;
                                     Identifying an insulin receptor signaling modulator, useful as drug targets for treating diabetes or metabolic disorders, comprises contacting an assay system comprising insulin receptor signaling modifiers with a test agent.
                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                     12-JAN-2001;
12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         studying intracellular protein networks and a protein source for screening proteins for binding low molecular weight drugs. The human protein coding sequence is useful for gene diagnosis and gene therapy, expression vectors and transformant cells for detection of ligands and
                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               WO200255664-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human insulin receptor signaling modifier SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA018510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAO18510 standard; protein;
                                                                                                                         Seidel-Dugan C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n; insulin receptor signaling; insulin receptor signaling modifier;
diabetes; metabolic syndrome; antidiabetic.
                                                                                                      2002-599664/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGAGAARGRASWCWALALLWLAVVPGW 29
                                                                                                                                                                                      2001US-0261518P.
2001US-0261531P.
2001US-0261532P.
2001US-0261589P.
2001US-0261590P.
2001US-0261694P.
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2001US-0261697P.
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2001US-0261461P.
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2001US-0261457P.
2001US-0261458P.
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                                                                                                                                               INC.
                                                                                                                         Ferguson
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Pred. No. 26;
                                                                                                                          Kidd
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Disclosure;

Page 134-135; 232pp; English.

invention relates to a method of identifying a candidate

preventing immune system, de neurological, pulmonary and

developmental, eye, nd cardiac disorders,

cancer, or parasitic

smooth muscle

present

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ABG32373
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AC ABG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                   09-FEB-2001; 2001US-0268113P.
15-FEB-2001; 2001US-0269215P.
27-FEB-2001; 2001US-0272271P.
07-MAR-2001; 2001US-0274491P.
09-MAR-2001; 2001US-0274473P.
23-MAR-2001; 2001US-0278479P.
                                                                                                                                                                                                                           Sanjanwala I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insulin receptor (INR) signaling modulating agent, involving contacting an assay system comprising an insulin receptor signaling modifier (ISM) polypeptide or nucleic acid with a test agent, and detecting a test agent biased activity of the assay system. The method is useful for identifying candidate INR signaling modulating agents. ISM genes may be used as drug targets for treatment of disorders related to INR signaling such as diabetes or metabolic syndrome. ISM nucleic acids and polypeptides are useful for identifying and testing agents that modulate ISM function and for other applications related to the involvement of ISM in INR signaling, and for identifying subjects having a predisposition to such diseases associated with INR signaling. The present sequence is an ISM protein described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         smooth muscle disorder; lactic acidosis; neurological disorder; parkinson's disease; cardiac disorder; congentive heart failure; myocardial infarction; pulmonary disorder; emphysema; bronchitis; parasitic infection; amoebiasis; filariasis; cancer; leukaemia; cell proliferative disorder; Incyte 2900469CD1; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; NZMS-3; immune system disorder; AIDS; contact dermatitis; acquired immune deficiency syndrome; Chediak-Higashi syndrome; acquired immune deficiency syndrome; Chediak-Higashi syndrome; common variable immunedeficiency; developmental disorder; cataract; Cushing's syndrome; hypothyroidism; eye disorder; glaucoma; asthma; metabolic disorder; cystic fibrosis; sickle-cell anaemia; epilepsy; smooth musella disorder; cystic fibrosis; sickle-cell anaemia; epilepsy;
                             New isolated human enzymes (NZMS), useful for diagnosing, treating and preventing immune system, developmental, eye, metabolic, smooth muscle
                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-FEB-2002; 2002WO-US003814.
                                                                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2002.
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                                                                                                                                              2002-643488/69.
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                                                                                                                                                                                                la MM, Lu
Yue H,
Lal PG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                Lu Y, Lee
H, Yao MG,
PG, Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NZMS-3,
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                                                                                                                                                                                                Lee S, Thorni
Swarnaker A,
                                                                                                                                                                                                                                                        EA,
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Pred. No. 2
                                                                                                                                                                                                                              Hafalia AJA, V
S, Thornton M,
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                                                                                                                                                                                                      Jones
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                                                                                                                                                                                                                              Warren BA,
M. Walia NK,
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                                                                                                                                                                                                Baughn
Xu Y;
HZ;
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infections.

Claim 1; Page 149-150; 170pp; English.

The invention relates to a new isolated human enzyme (NZMS) (I) and the encoding nucleic acid (II). The polypeptides and polynucleotides are useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NZMS. The NZMS or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The antibody is useful in diagnosing a condition or disease associated with the decreased expression or NZMS and in detecting (I). (I) is useful in the production of antibodies. The microarray is useful in monitoring or measuring gene expression profiles. The polypeptides and polynucleotides are useful in diagnosing, treating and preventing diseases or conditions a simunate system disorders (e.g. acquired immune deficiency syndrome (AIDS), contact dermatitis), immune deficiencies (e.g. common variable immunodeficiency, Chediak-Higashi syndrome), developmental disorders (e.g. Custing's syndrome, hypothyroidism), eye disorders (e.g. glaucoma, cataract), metabolic disorders (e.g. cystic fibrosis, sickle-cell anaemia), smooth muscle disorders (e.g. cystic fibrosis, sickle-cell encurological disorders (e.g. parkinson's disease, epilepsy), cardiac disorders (e.g. parkinson's disease, epilepsy), cardiac disorders (e.g. parkinson's disease, epilepsy), cardiac (amobiasis, filariasis), and cell proliferative disorders (e.g. cancer, protein interactions, drug-target interactions, and gene expression of 11 novel human enzymes (NZMS1-11) of the invention

Sequence 371 AA;

Query Match

32.8%; Score 55.5; DB 5; Length 371;

Best Local Similarity 55.6%; Pred. No. 26;

Matches 15; Conservative 0; Mismatches 5; Indels 7; Gaps

:3 •

3 RGAGAARGRASWCWALALLWLAVVPGW 29

sarch completed: June 8, 2004, 14:03:57
bb time : 8.95833 secs

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inimum DB
aximum DB
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Maximum Match 10
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seq length: 0 seq length: 2000000000
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Match
hits satisfying chosen parameters:
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169
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Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-252-991A-32898
US-09-252-991A-16705
US-09-252-991A-23299
US-09-252-991A-23199
US-09-252-991A-27810
US-09-252-991A-27810
US-09-252-991A-27810
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US-09-252-991A-27810
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US-09-252-991A-23997
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                18062, A
26303, A
27451, A
275, App
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28, Appl
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32898, A
2, Appli
16705, A
16705, A
216705, A
23296, Appl
274, Appl
274, Appl
290, Appl
290, Appl
4, Appli
4, Appli
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16906, A
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Sequence 16506, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 16906
LENGTH: 263
TYPE: PRT

US-09-252-991A-16906

Qy 12 Db 27	Query Match Best Local : Matches	28 49.5 29.3 248 4 US 29 49.5 29.3 303 4 US 30 49 29.0 1498 4 US 31 49 29.0 1498 4 US 32 48.5 28.7 534 4 US 33 48.5 28.7 534 4 US 34 48 28.4 170 4 US 35 48 28.4 222 4 US 36 48 28.4 229 4 US 37 48 28.4 29.4 US 38 48 28.4 29.4 US 40. 48 28.4 495 4 US 41 48 28.4 495 4 US 42 48 28.4 1421 4 US 43 48 28.4 1421 4 US 43 48 28.4 1421 4 US 44 48 28.4 1421 4 US 45 47.5 28.1 191 4 US 45 47.5 28.1 191 4 US 45 47.5 28.1 191 4 US 45 10.0 6551795 GENERAL INFORMATION: APPLICATION WIGHER: US/09 PATOR FILING DATE: 1990-02-18 FRIOR APPLICATION NUMBER: US/09 FRIOR FILING DATE: 1990-02-18 PRIOR PRIOR PRI US/09 TYPE: PRT ORGANISM: PSeudomonas aeruginos
ASWCWALALLWLAVVPGWS	32. Similarity 42. 8; Conservative	SS SQ P PRHAMENTANS 10 S DHUHACHENAPH' 1 44 HAHAH PHHHHA 4 NANANANANANANANANANANANANANANANANANA
LWLAVVPO TWPACSSA	32.5% 42.1% vative	3 248 4 US- 3 303 4 US- 3 303 4 US- 0 1498 4 US- 0 1498 4 US- 7 251 4 US- 251 4 US- 4 170 4 US- 4 229 4 US- 4 229 4 US- 4 290 4 US- 4 1495 4 US- 4 1495 4 US- 4 1421 4 US- 1 191 5 US- 1 191 6 US- 1 1
WS 45	Score 55; DB 4; Length 10Pred. No. 2;Mismatches 9; Indels	-09-134-001C-5085 -09-252-991A-17179 -09-252-991A-25696 -09-252-991A-27585 -09-252-991A-27585 -09-252-991A-25102 -09-148-545-135 -09-252-991A-22195 -09-252-991A-22195 -09-252-991A-1336 -09-489-039A-10528 -09-489-039A-10528 -09-489-039A-10528 -09-252-991A-17805 -09-252-991A-25365 -09-252-991A-25365 -09-252-991A-25365 -09-252-991A-25365 -09-252-991A-25365 -09-252-991A-25365 -09-252-991A-25365 -09-252-991A-25365 -09-252-991A-25365
	109; els 0; Gaps 0;	Sequence 5085, Ap Sequence 17179, A Sequence 27585, A Sequence 31234, A Sequence 27585, A Sequence 17265, A Sequence 17265, A Sequence 26306, A Sequence 25105, A Sequence 25102, A Sequence 135, App Sequence 1480, A Sequence 19602, A Sequence 1333, A Sequence 17805, A Sequence 17805, A Sequence 27855, A

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                                                                                                                             US-09-220-528-104
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                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 104
LENGTH: 215
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LENGTH: 74
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                                                               Matches
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EARLIER FILING DATE: 1998-12-22
EARLIER APPLICATION NUMBER: 60/108,148
EARLIER FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/163,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                        EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 120
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/220,528A CURRENT FILING DATE: 1998-12-24
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SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Milbrandt, Jeffr
APPLICANT: Baloh, Robert H.
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor FILE REFERENCE: 6029-7998
                                                                                                                                          TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                              Similarity
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QRGRGAAACARSWCRCARSAWATAPTSW 100
                             RRGAGAARGRASWCWALALLWLAVVPGW 29
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nilarity 35.7%;
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Conservative
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Pred. No. 2.
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Pred. No. 5.9;
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US-09-252-991A-32898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Patent No. 5310880
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-683-957B-2
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LENGTH: 228
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                 TELEFAX: (202) 833-87 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acid
                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MacLaugh
TITLE OF INVENTION:
TITLE OF INVENTION:
TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 466-0800
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                   NAME: Goldstein, Jorge A. REGISTRATION NUMBER: 29,0
                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 199104: CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 New CITY: Washington
                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                  TELEPHONE:
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1100 New York Avenue, N.W.
                                                 575 amino acids
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protein
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                                                                                   <u>ب</u>
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Pred. No. 8.1;
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S-07-683-957B-2

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ORGANISM: Pseudomonas aeruginosa $-09-252-991A-16705
                                                                                                                 Query Match
                                                                                                                                                                                                        SEQ ID NO 19862
LENGTH: 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19862, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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LENGTH: 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-252-991A-19862
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ESEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
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                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                                               Local
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191 RRGAGRGRGRSGACDGLA 208
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61.1%;
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Pred. No. 25;
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RESULT 11
US-09-252-991A-27810
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US-09-252-991A-23296
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NUMBER OF SEQ ID NOS:
SEQ ID NO 21199
LENGTH: 194
                                                                                                                 GENERAL INFORMATION:
                                                                                                                                    Sequence 27810, A
Patent No. 655179
                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local
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                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                     FILE REFERENCE: 107196.136
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; Pred. No. 5.6;
5; Mismatches
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; SOFTWARE: FastSEQ for Windov
; SEQ ID NO 22
; LENGTH: 85
; TYPE: PRT
: ORGANISM: Escherichia coli
JS-09-431-705-22
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JS-09-205-258-274
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LENGTH: 370
TYPE: PRT
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GENERAL INFORMATION:
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EARLIER APPLICATION NUMBER: PCT/US98/11422
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 06132/060001
CURRENT APPLICATION NUMBER: US/09/431,705
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 52
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TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: vaccination against helicobacter infection
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                            FILE REFERENCE: PZ007Pl
                                                                                                                                                                                                                                                     APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
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                                                                                                                                             APPLICATION NUMBER: 60/048,885 FILING DATE: 1997-06-06
                                                                             APPLICATION NUMBER: 60/048,881 FILING DATE: 1997-06-06
                                                                                                                          APPLICATION NUMBER: 60/049,375
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 APPLICATION
                            FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,896
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o. 6585975
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NUMBER: 60/049,020
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SEQ ID NO 274
LENGTH: 88
                               EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
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                                                                               ER APPLICATION NUMBER: 60/094,657
                                                                                                                                                                                                                       APPLICATION NUMBER: 60/0
PTI ING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,883
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/048,916
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
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APPLICATION NUMBER: 60/048,875
                                                                                                           APPLICATION NUMBER:
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APPLICATION NUMBER: 60/049,019
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APPLICATION NUMBER: 60/048,892
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APPLICATION NUMBER: 60/048,900
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,882
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APPLICATION NUMBER: 60/048,971
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APPLICATION NUMBER: 60/048,876
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ORGANISM: Homo sapiens

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Query Match
Best Local Similarity
Warches 9; Conserva
          CURRENT APPLICATION NUMBER: US/09/364,425B
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/094,879
PRIOR FILING DATE: 1998-07-31
PRIOR APPLICATION NUMBER: 60/106,300
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/110,906
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR APPLICATION NUMBER: 60/121,851
PRIOR FILING DATE: 1999-02-26
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S-09-170-496D-290
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S-09-170-496D-290
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APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Humar G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICANTION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SQFTWARE: PatentIn version 3.1
SEQ ID NO 290
LENGTH: 1310
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESULT 15
S-09-364-425B-55
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Lowitz, Kevin P.
APPLICANT: Chen, Ruoping
TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled Orphan Rece
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 290, Application US/09170496D Patent No. 6555339 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55, Application US/09364425B Patent No. 6653086
NUMBER OF SEQ ID NOS: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (88)
OTHER INFORMATION: Xaa equals stop translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (53)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Search completed: June Job time: 2.33333 secs
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                                                                                   Query Match
Best Local Similarity 52...
Conservative
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SEQ ID NO 55
LENGTH: 1310
TYPE: PRT
                                                    907 QASWCHARRLVWLHSAP 923
                                                                            11 RASWCWALALLWLAVVP 27
           8, 2004, 14:09:16
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| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 2218. Ap	Sequence 3, Appli	Sequence 13, Appl	Sequence 60, App.	Sequence 300, App	Sequence 198, App	Sequence 8, Appl.	Sequence 240, App	Sequence 269, App	Sequence 167, App	Sequence 11538, A	Sequence 126, App	Sequence 2, Appli.	Sequence 126, App	Sequence 2, Appli	Description	

Sequence 126, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 95 Human secreted proteins

45	44	43	42	41	40	9	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
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ALIGNMENTS

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NAME/KEY: SITE
LOCATION: (246)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
S-10-653-595-126
S-10-010-050A-2
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PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/078,578
                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10010050A Publication No. US20020173624A1 GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 126
LENGTH: 346
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                                                                                                                                                                                                                                                         APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
CURRENT APPLICATION NUMBER: US/10/010,050A
CURRENT FILING DATE: 2002-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10-010-050A-2
                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/053,613
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/122,383 PRIOR FILING DATE: 1998-07-24
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,573
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PRIOR APPLICATION NUMBER: US 09/397945
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: PCT/US99/05804
PRIOR FILING DATE: 1999-03-18
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CURRENT APPLICATION NUMBER: US/10/653,595
CURRENT FILING DATE: 2003-09-03
            ORGANISM: Homo sapien
                                              LENGTH: 346
TYPE: PRT
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OTHER INFORMATION: Xaa equals any of the naturally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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APPLICATION NUMBER: 60/078,574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 169; DB 12; ilarity 100.0%; Pred. No. 3.8e-12; Conservative 0; Mismatches 0;
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                                                                  Matches
                                                                                Query Match
Best Local
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                                                                                                                                                             LOCATION: (242)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (246)
OTHER INFORMATION: X
NAME/KEY: SITE
LOCATION: (347)
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Best Local
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PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
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PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
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PRIOR APPLICATION NUMBER: 60/078,576
PRIOR FILING DATE: 1998-03-19
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CURRENT FILING DATE: 1999-09-17
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                                                                                                                                                                                                                                                                              NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                DRGANISM: Homo
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                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/078,581
FILING DATE: 1998-03-19
APPLICATION NUMBER: 60/078,577
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30; Conservative
                         MRRGAGAARGRASWCWALALLWLAVVPGWS
MRRGAGAARGRASWCWALALLWLAVVPGWS 30
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5. US20030065139A1
                                                                 Conservative
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                                                                              100.0%;
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                                                                 Mismatches
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                                                                                                                                                                                                                                        of the naturally occurring L-amino acids
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                                                                                               DB 12;
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                                                                 Indels
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ORGANISM: Streptomyces avermitilis
3-10-156-761-11538
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Best Local Similarity
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PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11538
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Patent No. US20020058306A1
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Publication No. US20030119018A1
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CURRENT FILING DATE: 2001-03-16
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APPLICANT: SAKAKI, YOSHIYUMI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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APPLICANT:
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PRIOR FILING DATE: 2000-03-16
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TITLE OF INVENTION: No. US20020058306Alel G Protein-Coupled Receptors
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            APPLICATION NUMBER: 60/192,155
FILING DATE: 2000-03-24
APPLICATION NUMBER: 60/192,935
FILING DATE: 2000-03-29
                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/192,916
FILING DATE: 2000-03-29
APPLICATION NUMBER: 60/192,923
                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-03-16
APPLICATION NUMBER: 60/192,945
FILING DATE: 2000-03-29
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                                                                                              APPLICATION NUMBER: 60/192,234
FILING DATE: 2000-03-27
                                                                                                                                                          APPLICATION NUMBER: 60/192,830
                                                                                                                                                                                  APPLICATION NUMBER: 60/192,933 FILING DATE: 2000-03-29
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167 RGAGSSTKLYATKNLTELIGVYGSRYGGDKSSWSWAGGLIWLAPRARW 215
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SEQ ID NOS:
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HORIKAWA, HIROSHI
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Pred. No. 23;
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US-10-291-265-269
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US-09-811-284-167
                                                              SEQ ID NO 240
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 127
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LENGTH: 192
                                                                                                          APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prote
FILE REFERENCE: DEX-0291
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR TILING DATE: 2000-11-22
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APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
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                                                                               NUMBER OF SEQ ID NOS: 284
SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR APPLICATION NUMBER: 09/633,870
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APPLICANT: Tang et al
TITLE OF INVENTION: NO. US20030232054A1el Nucleic Acids and Polypeptides
EILE REFERENCE: 21272-017 (785)
CURRENT APPLICATION NUMBER: US/10/291,265
CURRENT FILING DATE: 2000-01-25
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NUMBER OF SEQ ID NOS: 944
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2000-01-25
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                       ENGTH: 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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Local Similarity 39.3%;
les 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 GAGAARGRASWCW-----ALALLW 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKAAVRGRPCWCWPCQPALLVSIIALVW 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.2%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
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Pred. No. 12;
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Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 15;
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US-09-989-920-240

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LENGTH: 214
TYPE: PRT
ORGANISM: Mycobacterium leprae
S-10-080-170-198
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CURRENT APPLICATION NUMBER: US/10/084,846A

CURRENT FILING DATE: 2003-02-25

PRIOR APPLICATION NUMBER: PCT/EP01/09815

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-02-25

NUMBER OF SEQ ID NOS: 120

SOFTWARE: Patentin Ver. 3.2
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              Query Match
Best Local Similarity
     Matches
                                                                                                                                     SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 198
                                                                                                                                                                                                                                                                                                                                                     3-10-080-170-198
Sequence 198, Application US/10080170
Publication No. US20030129601A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: COLE, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPH TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES FILE REFERENCE: 03495.0218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                       NUMBER OF SEQ ID NOS: 652
                                                                                                                                                                                   CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/080,170 CURRENT FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TREFZER, AXEL
APPLICANT: BECHTHOLD, ANDREAS
TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WEITNAUER, GABRIELE APPLICANT: MUHLENWEG, AGNES APPLICANT: TREFZER, AXEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 19608
TYPE: PRT
OCCUPATION: Streptomyces viridochromogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 12; Conserv
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No. US20040006026A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGGAGAGSWVWMGGWGGGAGALWVAVVGG 49
   Conservative
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                33.1%;
41.7%;
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              Score 56;
Pred. No.
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Pred. No. 1.8e+03;
3; Mismatches 11
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Pred. No.
 Mismatches
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                                DB 14;
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11;
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                                Length 214;
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Indels
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Gaps
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; ORGANISM: Homo sapiens US-10-092-900A-300
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US-10-092-900A-300
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                                                Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 768
SEQ ID NO 300
LENGTH: 403
                                                                                                                                                                                                                                                                                                                                            APPLICAN: Burges, Catherine E.

APPLICAN: Burges, Catherine E.

TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding FILE REFERENCE: 21402-290C

CURRENT APPLICATION NUMBER: USSN 60/274,322

PRIOR APPLICATION NUMBER: USSN 60/274,322

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: USSN 60/283,675

PRIOR APPLICATION NUMBER: USSN 60/283,675

PRIOR FILING DATE: 2001-04-13

PRIOR FILING DATE: 2001-04-13

PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: USSN 60/338,092

PRIOR FILING DATE: 2001-12-03

PRIOR APPLICATION NUMBER: USSN 60/274,281

PRIOR PRIOR ENGLISHED STOREN 60/274,281

PRIOR PRIOR ENGLISHED STOREN 60/274,191
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                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: USSN 60/279,995
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: USSN 60/274,191
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: USSN 60/325,681
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-09-27
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APPLICANT:
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                                                                                                                           PRIOR FILING DATE: 2001-04-30
                                                                                                                                                                      PRIOR FILING DATE: 2001-05-3:
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                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: USSN 60/304,354
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                                                                                                                                               APPLICATION NUMBER: USSN 60/287,424
                                                                                                                                                                                      APPLICATION NUMBER: USSN 60/294,899
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Leite, Mario W.
Zhong, Haihong
Alsobrook, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Casmu. valerie
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Rieger, Daniel K.
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Fernandes, Elma
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Gangolli, Esha A.
Vernet, Corine A.M.
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Kekuda, Ramesh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xiaojia Sasha
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Same

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NUMBER
SOFTWARE:
SEQ ID NO 13
                                                                                                                                                                 Patent No. US20020155552A1
GENERAL INFORMATION:
APPLICANT: Beroman
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                    APPLICANT: Bergmann, Johanna
TITLE OF INVENTION: "PRIONINS", HIGHLY SPECIFIC MARKERS FOR NONINVASIVE PRE-SYMPTON
TITLE OF INVENTION: DETECTION OF TSE DISEASES AND TARGETS FOR THERAPEUTIC REAGENTS
TITLE OF INVENTION: CONTROL TSE DISEASES IN ANIMALS AND HUMANS
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
SEQ ID NO 60
                                                  CURRENT APPLICATION NUMBER: US/09/242,4500
CURRENT FILING DATE: 2000-02-16
NUMBER OF SEQ ID NOS: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mihoro SAEKI
TITLE OF INVENTION: Human Proteins and cDNAs thereof
EILE REFERENCE: 2001-1102A/MMC/00653
CURRENT APPLICATION NUMBER: US/09/890,688
CURRENT FILING DATE: 2001-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, Application US/09890688 Publication No. US20030144475A1
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PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: JP 11-34684
PRIOR FILING DATE: 1999-12-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 160
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ORGANISM: Homo sapiens
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FILING DATE: 2000-02-08
APPLICATION NUMBER: JP 2000-34091
FILING DATE: 2000-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-03-14
APPLICATION NUMBER: JP 2000-160851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 2000-71161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 2000-34090 FILING DATE: 2000-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 2000-35899
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Pred. No. 91;
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Pred. No.
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1; Mismatches
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SEQ ID NO 3

; LENGTH: 65

; TYPE: PRT

; ORGANISM: homo sapiens
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                                                                                                                                                                                                                                                                                                                                                           Sequence 2218, Application US/10094749 Publication No. US20030219741A1
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APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09242450A Patent No. US20020155552A1
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TITLE OF INVENTION: "PRIONINS", HIGHLY SI
TITLE OF INVENTION: DETECTION OF TSE DISI
TITLE OF INVENTION: CONTROL TSE DISEASES:
TITLE OF INVENTION: CONTROL TSE DISEASES:
TITLE OF INVENTION: CONTROL TSE DISEASES:
TITLE OF INVENTION: CONTROL TSE DISEASES:
TITLE OF INVENTION NUMBER: US/09/242,450A
CURRENT FILING DATE: 2000-02-16
UNMBER OF SEQ ID NOS: 13
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ORGANISM:
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LOCATION: (1)..(28)
OTHER INFORMATION: membrane spanning helix of CJAS from amino acid 25 to amino
OTHER INFORMATION: 52 in the complete sequenc
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                                                                                                                HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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                                                                                                                                                                                                                                                                                                           TOMOYASU
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Pred. No. 41;
1; Mismatches
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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28.7	28.7	28.7	28.7	28.7	28.7	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.3	29.3	29.6
688	435	276	210	125	111	1221	755	317	250	188	139	118	519	310	529
N	N	N	N	N	N	N	2	N	N	2	N	N	N	N	Ν
B97152	A12082	B82243	S36297	C83138	T14306	E83327	B75346	T35010	AB1555	B82183	A71123	S52855	S75570	T16233	B98227
probable membrane	hypothetical	hypothetical	T-cell receptor ga	hypothetical prote	glycine-rich prote	conserved hypothet	probable competenc	probable integral	ABC transporter tr	ankB protein	hypothetical	hypothetical	apolipoprotein N-a	hypothetical prote	cytochrome d oxida

ALIGNMENTS

A;Cross-references: GB:AL591985; PIDN:CAC49196.1; PID:g15140681; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlo
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K. C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: D95941
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kD pSymB megaplasmid from the N2-fixing endos A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95941 RESULT D95941 ; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; A;Title: Genome sequence of Halobacterium species NRC-1. A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: C84390 RESULT 1 C84390 A;Cross-references: C;Genetics: A;Status: preliminary A;Molecule type: DNA A;Residues: 1-412 <KUR> 밁 Ş A; Gene: A; Molecule type: DNA A; Residues: 1-606 <STO> C;Accession: C84390
R;NG, W.V.; Kennedy, S.P.; Mahairas, sulfate transport system permease protein [imported] - Halobacterium sp. NRC-1 C;Species: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 conserved hypothetical membrane protein, paralogue of Y20848 SMb21292 [imported] A;Status: preliminary Matches Best Local Query Match N cysT1 508 RALGASRGRALWDVELPLVWPGVVAG 533 3 RGAGAARGRASWCWALALLWLAVVPG 28 Similarity Conservative GB:AE004437; NID:g10581803; PIDN:AAG20487.1; GSPDB:GN00138 39.1%; 2, Score 66; D Pred. No. 0. Mismatches G.G.; Berquist, B.; DΒ uist, B.; Pan, M.; Shukla, H.D.;
M.J.; Hough, D.W.; Maddocks, D.(2 10; Length 606; Indels Ebhardt, H.; Lowe, ; E.; Komp, C.; Lelaure,
D.H.; Wong, K.; Yeh, K.(N.A.; Fisher, Gaps F.; Barloy-Hubler, N.A.; Fisher, R.F.; 0; D.G.; G.; Jablor T.M.; Lia ı Sinor

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#Risperimental Source: Strain pasc

#Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

riones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

B-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

#B-Neto (BenBank, June 2000)

#Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

#Properimental Source: Strain pasc

#Properimental Source: Strain pasc

#Properimental Source: Strain pasc

#B-Neto (B-D.; Camargo, M.C.; Ferreira, A.J.S.)

#B-Neto (B-D.; Franca, S.C.; Franco, M.C.; Frohm

#Properimental Source: Strain pasc

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Accession: F82729
;janonymous, The Xylella fastidiosa Consortium of the Organization for Nuclectide lature 406, 151-157, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: The composite A; Reference number: A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;Accession: F82729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable integral membrane protein [imported] - Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:AE003942; GB:AE003849; NID:g9105990; PIDN:AAF83864.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2968c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Note: MLCB1243.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Residues: 1-214 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Status: preliminary; translated from GB/EMBL/DDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T44701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Reference number: Z22830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:AL023635; PIDN:CAA19188. Experimental source: cosmid B1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Species: Mycobacterium leprae
;Date: 21-Jan-2000 #sequence_r:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-232 <SIM>
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10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTSAIARGIYQWRWSIATLWFITV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGAGAARGRASWCWALALLWLAVV 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AARGRASWCWA-----LALLWLAVVP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANKGRPTWTWLATVLLFIAIMWLSTVP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ite genome of the legume symbiont Sinorhizobium meliloti. A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _revision 21-Jan-2000 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6;
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Pred. No. 4.4;
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Pred. No. 3
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3.1;
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A;Experimental source: strain 9a5c

A;Experimental source: strain 9a5c

A;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M. Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, M.L.; Kemper, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below A;Accession: A82729 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB: AE003942; GB: AE003849; NID: g9105990; PIDN: AAF83859.1; GSPDB: GN0012
                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-284 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; anonymous, The Xylella Nature 406, 151-157, 2000
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A;Title: Alternatively spliced Hox-1.7 transcripts encode
A;Reference number: A48428; MUID:92190539; PMID:1983703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: unassigned homeobox prote
C;Keywords: DNA binding; homeobox; nucle
F;94-150/Domain: homeobox homology <HOX>
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A; Residues: 1-159 < RUB>
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DNA Seq. 1, 115-124, 1990
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C;Superfamily:
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A;Contents: annotation
C;Genetics:
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Pred. No. 7
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Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins;
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Gontents:

annotation

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Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; age, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T. Karp, P.; Romero, P.; Zhang, S. Hence 294, 2317-2323, 2001
Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mserved hypothetical protein Atu2314 (imported] - Agrobacterium tumefaciens
Species: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ullulanase secretion protein pull - Klebsiella pneumoniae
;Specites: Klebsiella pneumoniae
;Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change
                                                                                                         Query Match
                                                                                                                                                Map position:
                                                                                                                                                                                                    Cross-references: GB:AE008688; PIDN:AAL43303.1;
Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                   Residues:
                                                                                                                                                                                                                                                                                                                   Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58 Reference number: AB2577; MUID:21608550; PMID:11743193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: AI2860
                                                                                                                                                                                                                                                               Molecule type: DNA
                                                                                                                                                                                                                                                                                      Status: preliminary
                                                                                                                                                                                                                                                                                                           Accession: AI2860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:X52462; NID:g43917; Experimental source: strain UNF5023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pugsley, A.P.; Reyss, I.

11. Microbiol. 4, 365-379, 1990

12. Title: Five genes at the 3' end of the Klebsiella pneumoniae

13. Reference number: S11799; MUID:90286914; PMID:2162463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Gene: XF1049
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                                                                                                                                                                     Atu2314
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                                                                  Similarity
8; Conserv
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                          AARGRASWCWA-----LALLWLAVVP 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRGKMRAWQAWCDSLGLSVLALTPDVLALPHSPTGWS 154
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                                                                                                                                            circular chromosome
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                                                               7; Mismatches
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Pred. No. 18;
3; Mismatches
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                                                                                  Score 53; DB Pred. No. 19;
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Pred. No. 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   D.; Chen, L.; Wood, G.E.; Chen, D.; Kutyavin, T.; Levy, R.; Li, N
                                                                                                   2
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                                                                                                                                                                                                                      PID:g17740794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Woo,
C;Species: Bos primigenius taurus (cattle)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 01-Dec-2000
C;Accession: A01398; B01398
R;Cate, R.L.; Mattaliano, R.J.; Hession, C.; Tizard, R.; Farber, N.M.; Cheur an, K.L.; Ragin, R.C.; Manganaro, T.F.; MacLaughlin, D.T.; Donahoe, P.K. cell 45, 685-698, 1986
                                                                                                                           mullerian inhibiting factor precursor - bovine N; Alternate names: Mullerian inhibiting substance
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21

GAQRIRSAWIFLAPTLIVLAIVAGW

RESULT 11

the bovine and

human

genes for Muellerian

inhibiting

substance

R.; Farber, N.M.; Cheung, D.T.; Donahoe, P.K.

A.; Ninfa

(MIS)

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C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AG3627
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc Proc. Matl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensi A; Reference number: AD3252; PMID:11756688
8
                                                                                                                           A; Map position:
                                                                                                                                                                                  A; Experimental source: strain 16M
                                                                                                                                                                                                 A; Cross-references: GB: AE008918; PIDN: AAL54186.1;
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-220 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                maltose transport system permease protein malF [imported] - Brucella melitensis C;Species: Brucella melitensis
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A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz,
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H97637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002 C;Accession: H97637
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A;Residues: 1-428 <KUR>
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                                                                                   Query Match
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Best Local
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                                                             Similarity
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GAARGRASWCW-ALALLWLAVVPGW
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                                          Conservative
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                                                         31.1%;
48.0%;
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                                        5.
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                                                           Score 52.5;
Pred. No. 13;
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Pred. No.
                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
29
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ckelz, B.;
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C;Date: 28-May-1993 #sequence revision 28-May-1993 #text_change 17-Mar-2000 C;Accession: S30075; S48565 revision 28-May-1993 #text_change 17-Mar-2000 R;Dancis, A.; Roman, D.G.; Anderson, G.J.; Hinnebusch, A.G.; Klausner, R.D. Proc. Natl. Acad. Sci. U.S.A. 89, 3869-3873, 1992 A;Title: Ferric reductase of Saccharomyces cerevisiae: Molecular characteri: A;Reference number: S30075; MUID:92237270; PMID:1570306 A;Accession: S30075
                 A; Residues: 1-686 < I
A; Cross-references:
₹;Pauley,
                                                                                                                                                                                                                                                              ferric reductase (EC 1.6.99.-) FRE1 - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 15-575 <CA2>
C;Comment: This glycoprotein, produced by the Sertoli cells of the testis, causes regres tissues of Mullerian duct origin. Other roles for this protein in gonadal differentiati ter duct regression and in the adult ovary.
C;Comment: This protein is homologous to the beta transforming growth factor, inhibin all these sequences. All of these proteins are biologically active as disulfide-linked diment; Comment: Although it does not compete with EGF for receptor binding sites, MIS can inh C;Superfamily: inhibin
                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                 S30075
                                                                                                                                                                                                                                                                                                                                                         RESULT
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A; Note: sequence extracted from NCBI backbone
C; Superfamily: fruit fly frizzled protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; J. Biol. Chem. 267, 25202-25207, 1992
A;Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely A;Reference number: A45054; MUID:93094228; PMID:1334084
A;Accession: A45054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable intercellular signal transducer or transmitter Fz-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1
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A;Accession: A01398
A;Molecule type: DNA
A;Residues: 1-14 <CAl>
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A; Residues: 15-575 < CA2>
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                                       1-686 <DAN>
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    EMBL: M86908; NID: g171520; PIDN: AAA34608.1; PID: g171521
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Pred. No. 36;
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Pred. No. 28
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Riffinan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; He Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A; Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing A; Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                   C;Species: Sincrhizobium medilori
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change
C;Accession: E95984 #sequence_revision 24-Aug-2001 #text_change
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain. P.;
A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                              conserved hypothetical membrane protein, paralogue
C;Species: Sinorhizobium meliloti
                                             A; Accession: E95984
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C;Keywords: cornea
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A;Title: CDNA analysis predicts a cornea-specific collagen. A;Reference number: A38587; MUID:91142213; PMID:1705041
A;Accession: S16501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Gallus gallus (chicken)
C;Date: 14-Feb-1992 #sequence revision 15-Aug-1997 #text_change 15-Sep-2003
C;Accession: S16501; A38587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-174, 'X',
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A; Residues: 1-1146 < MAR>
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A;Map position: 12R
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C;Keywords: oxidoreductase; transmem
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C; Genetics:
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A; Residues: 1-686 < P;
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41.7%;
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Pred. No. 4;
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                                                                                                                     Vorholter, F.J.; Hernand
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laximum DB seq length: 2000000000
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Maximum Match 100%
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Copyright (c) 1993 - 2004 Compugen Ltd.
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P28678 drosophila
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Q8xzr2 ralstonia s
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EMBL; AF068227; AAC27614.1; Genew; HGNC:2076; CLN5. MIM; 608102;	by non- lfied and lties required	SWISS-PROT entry is copyright. It is produced through a collaboration on the Swiss Institute of Bioinformatics and the EMBL outstation uropean Bioinformatics.	ipofuscinos ac.uk/nc1/C	-!- DATABASE: NAME=NCL CLN5;	The first symptom is motor clumsin visual failure, mental and motor	progressive visual and mental decline, motor disturbance, epilepsy	also known as ceroid lipofuscinosis neuronal 5 (CLNS). VLINCL is a	!- DISEASE: Defects in CLN5 are the cause of Finnish infantile neuronal ceroid linestrations (Transcription)	-i- PTM: Glycosylated.	ī ī	-!- FUNCTION: Not known.		localization of the neur	A., Peltonen I.	SUBCELLULAR LOCATION, AND GLYCOSYLATION. MEDLINE=21968572: DubMed=11971870.	[2]	ofuscinosis.	"CLN5, a novel gene encoding a putative transmembrane protein mutated	Peltonen L.;	62406;		M N.A., VARIANT VLINCL ASN-279. AND VARIANT ABC-36		Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo		CLN5.		8 (Rel. 37, Last	Created)	CLN5 HUMAN STANDARD; PRT; 407 AA.	RESULT 1

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RESULT 2
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Best Local !
                                                                                               HAMAP; MF_00454; -; 1.
InterPro; IPR003691; Camphor_CrcB
                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See ) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                              Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico I., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.", Nature 415:497-502(2002).
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28-FEB-2003
28-FEB-2003
                                                            Pfam; PF02537; CRCB; 1. TIGRFAMS; TIGR00494; crcB; 1.
                                        Transmembrane;
                                                                                                                                              EMBL; AL646064; CAD15035.1; -.
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28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
28-FEB-2003 (Rel. 41, Last
Protein crcB homolog.
CRCB OR RSC1333 OR RSC2855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21681879; PubMed=11823852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR IOCATION: Integral membrane protein SIMILARITY: Belongs to the crcB family.
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GO:0016021; C:integral to membrane; TAS.
GO:0008151; P:cell growth and/or mainten
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Lysosome; Glycoprotein; Neuronal
n; Polymorphism; Epilepsy.
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K -> R (17
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Pred. No. 1.4e-14;
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449702DIDC9BFEE4 CRC64;
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RESULT 3
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Interpro; IPRO0047; HTH Tambrepressr.
Pfam; PF00046; homeobox; 1.
Pfam; PF04617; Hox9 act; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00031; HTHREPRESSR.
PRODom: PD000010; Homeobox; 1.
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Best Local &
Matches 13
                                                       Transcription regulation.

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SEQUENCE 162 AA; 18661
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                                                                                                                                              ProDom; PD000010; Homeobox; SMART; SM00389; HOX; 1.
                                                                                                                    PROSITE; PS00027; HOMEOBOX 1; 1. PROSITE; PS50071; HOMEOBOX 2; 1.
                                                                                                                                                                                                                                                                 EMBL; X13536; CAA31887.1; -. HSSP; P02833; 9ANT.
                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Sequence-specific transcription factor which is part a developmental regulatory system that provides cells with specific positional identities on the anterior-posterior axis.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Belongs to the Abd-B homeobox family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last anotation update)
Homeobox protein Hox-A9 (Hox-1.7) (Fragment).
HOXA9 OR HOX-1.7.
Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Verte:
McMammalia; Butheria; Rodentia; Hystricognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996
01-OCT-1996
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                                                                                                      Homeobox; DNA-binding; Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                   InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       products.";
DNA Seq. 1:115-124(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Alternatively spliced Hox-1.7 transcripts encode different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rubin M.R., Nguyen-Huu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92190539; PubMed=1983703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HXA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P51783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAVPO
     12;
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 GVGAALG--AWLRWAFAVLWNAINP 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GAGAARGRASWC-WALALLWLAVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                      96
162 AA;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
100
126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                    155 ]
18661 MW;
             31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
  ω
••
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 56.5; DB; Pred. No. 1.3; 3; Mismatches
             Score 53.5;
Pred. No. 3.
                                                   HOMEOBOX.
; B84FA507EC67CF91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
; C2443FBAE5C81CB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Eute
Hystricognathi; Caviidae;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162
                                                                                                                                                                                                                                                                                                            moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                .9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
 9;
                                                                                                    Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
                                                    CRC64;
                         Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                    restrictions
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GAARGRASWCW---ALALLWLAVVPGW 29

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13

GSSRSRSSWCCNLKQLAFAGLAGDPAW 39

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RESULT 4
SPL_KLEPN
CD GSPL_K
                                                                                                                                                                                                                                                                                                                                 Best
                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
Bos taurus (Bovine).
Eukaryota, Metazoa; Cho:
Aammalia; Eutheria; Cett
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
                                                                                                                                                                                                   BOVIN
S LTD
                                                                                       MIS_BOVIN STANDARD; PRT; 575 AA. P03972; P03972; 23-OCT-1986 (Rel. 02, Created) 23-OCT-1986 (Rel. 02, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Muellerian inhibiting factor precursor (MIS) (Mullerian inhibiting substance).
                                                                                     AMH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M32613; AAA25134.1; -. EMBL; X52462; CAA36697.1; -. PIR; S11800; S11800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. Ther use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pugsley A.P., Reyss I.;
"Five genes at the 3' end of the Klebsiella pneumoniae pulcare required for pullulanase secretion.";
Mol. Microbiol. 4:365-379(1990)
-1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP. EXPORT OF PROTEINS. REQUIRED FOR THE TRANSLOCATION OF 1-1- SUBSCELULAR LOCATION: Inner membrane (Probable).
-1- SIMILARITY: BELONGS TO THE EXEL/PULL/OUTL/XCFY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P15751;
01-APR-1990
01-APR-1990
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 Transport; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF05134; GspL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel.
01-APR-1990 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90286914; PubMed=2162463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=UNF 5023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      General secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                            118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLEPN
                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                 4 GAGAARGRASWCWALALLWLAVVP-----GWS
                                                                                                                                                                                                                                                    GRGKMRAWQAWCDSLGLSVLALTPDVLALPHSPTGWS 154
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR007812; GspL.
                                                                                                                                                                                                                                                                                                                                                                          398 AA;
                                                                                                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumoniae.
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14, Last sequence update)32, Last annotation update)pathway protein L (Pullulanase)
                                  Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                        248
                                                                                                                                                                                                                                                                                                                                                                                         265 .
                                                                                                                                                                                                                                                                                                                                                                        44198 MW;
                                                                                                                                                                                                                                                                                                                             31.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                               ω
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                                                                                                                                                                                                                                                                                                                             Score 53;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                    ARG-RICH.
POTENTIAL.
; 72CF5D870EA99948 CRC64;
                                                                                                                                                                                                                                                                                                         ore 53; DB 1; Length 398; ed. No. 9.9; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA
                                                                                                         (Anti-muellerian hormone)
                                                                                                                                                                                                                                                                                   30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secretion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GSP) FOR THE N OF PULLULANASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pulc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL outstation
                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a collaboration
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00
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ON COOR DEPT DE
                                                                                                                                                                       RESULT 6
OPS1_DROPS
                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                 Query Match
Drosophila pseudoobscura (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7237;
                                                                                                                                            OPS1_DRO
P28678;
                                                                               01-DEC-1992 (Rel. 24, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Opsin Rh1 (Outer R1-R6 photoreceptor cells
                                                                                                                                                                                                                                                                                                                                                       CHAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
                                                                         NÎNAE OR RH1.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00438; GECYSKNOT.
ProDom; PD000357; TGFb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002400; GF Cys
InterPro; IPR001839; TGFb.
Pfam; PF04709; AMH N; 1.
Pfam; PF00019; TGF-beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M13151; AAA98765.1; -. PIR; A01398; WFBOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Homodimer; disulfide-linked.
-!- MISCELLANEOUS: Although it does not compete with EGF for recep binding sites, MIS can inhibit the autophosphorylation of the receptor in vitro.
-!- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cate R.L., Mattaliano R.J., Hession C., Tizard R., Farber N.M., Chow G., Ninfa E.G., Frey A.Z., Gash D.J., Chow E.P., Fisher R.P. Bertonis J.M., Torres G., Wallner B.P., Ramachandran K.L., Ragin R.C., Manganaro T.F., McLaughlin D.T., Donahoe P.K., "Isolation of the bovine and human genes for Mullerian inhibiting substance and expression of the human gene in animal cells.", Cell 45:685-698(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                           DROPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THIS GLYCOPROTEIN, PRODUCED BY THE SERTOLI CELLS OF THE TESTIS, CAUSES REGRESSION OF THE MUELLERIAN DUCT. IT ALSO IS ABLE TO INHIBIT THE GROWTH OF TUMORS DERIVED FROM TISSUES OF MUELLERIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DUCT ORIGIN.
                                                                                                                                                                                                                              41
                                                                                                                                                                                                                                                      4 GAGAARGRASWCWALALIWLAVVPG 28
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                            |:|| : | | : ||| || || GSGALIFQQAWDWPLSSLWL---PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR006799; AMH N.
IPR002400; GF_Cysknot.
                                                                                                                                                                                                                                                                                                                                          575 AA;
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                    25
477
503
507
540
                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                     24
575
541
572
574
540
                                                                                                                                                                                                                                                                                               31.1%;
                                                                                                                                                                                                                                                                                                                                          60623 MW;
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                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                Score 52.5;
Pred. No. 16
                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gonadal differentiation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                    MUELLERIAN INHIBITING FACTOR
                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                       892B89C11AC8B5A8
                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
                                                                                                                                                                                                                            62
                                                                                  cells opsin)
                                                                                                                                                       374 AA
                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                       CRC64;
                                                                                                                                                                                                                                                                                                           Length 575;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Farber N.M.,
E.P., Fisher R.A.,
                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL
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MBL outstation -
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Query Match
Best Local S
Matches 8
                                                                                                                      CARBOHYD
DISULFID
                                                                                               SEQUENCE
                                                                                                            BINDING
                                                                                                                                              DOMAIN
                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                              Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00237; GFCRRHODOPSN.
PROSITE; PS00237; G PROTRIN RECEP_F1_1;
PROSITE; PS00263; G_PROTRIN, RECEP_F1_2;
PROSITE; PS00238; OFSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                          Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00001; 7tm_
                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0012733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X65877; CAA46708.1; -. PIR; S40691; S40691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93012921; PubMed=1398053; Carulli J.P., Hartl D.L.; "Variable rates of evolution among Drosophila opsin genes."; Genetics 132:193-204(1992).
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000276; GPCR Rhodpsn.
InterPro; IPR001760; Opsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
STRAIN=Apple Hill;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linked to cis-retinal.
SUBCELLULAR LOCATION: Integral membrane protein.
PTM: Some or all of the carboxyl-terminal Ser or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Visual pigments are the light-absorbing molecules that mediate vision. They consist of an apoprotein, opsin, covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: Opsin Rh1 has an absorption maximum at 480 nm. SIMILARITY: Belongs to family 1 of G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: Each Drosophila eye is composed of 800
   166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Opsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ommatidia. Each ommatidium contains 8 photoreceptor cells the RI to R6 cells are outer cells, while R7 and R8 are in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ommatidia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                   P02699;
                                                  8
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphorylated.
ALGKIAYIWFMSTIWCCLAPVFGWS 190
                       ARGRASWCWALALLWLAVVP--GWS 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subfamily.
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191
215
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374 AA;
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                                                          30.8%;
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                                                                                                                                                                                                                                                                                                            protein; Transmembrane; Phosphorylation; n coupled receptor; Vision.
EXTRACELLULAR.
                                              7;
                                                        Score 52;
Pred. No.
                                                                                                                                                        5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                              N-LINKED (GLCNAC. .
                                                                                                                                            CYTOPLASMIC.
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5 (POTENTIAL).
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3 (POTENTIAL)
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2 (POTENTIAL).
                                                                                                                                                                                                                             4 (POTENTIAL).
                                                                                                                                                                                                                                           CYTOPLASMIC.
                                                                                                                    POTENTIAL
                                                                                            8228082D97E0FA34 CRC64;
                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                               Mismatches
                                                                                                         CHROMOPHORE
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                                                                    DB
                                                                   Length 374;
                                                                                                                               .) (PROBABLE).
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Piam; e.v... PRINTS; PR00489; FR1ZZLE, SMART; SM00063; FRI; 1.

FRIZZLED

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EMBL; L02529; AAA41173.1; -. InterPro; IPR000539; Frizzled. InterPro; IPR000024; Fz domain. InterPro; IPR000024; GPCR_secret Pfam; PF01534; Frizzled; 1. Pfam; PF01392; Fz; 1.
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELIULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Widely expressed. Most abundant in kidney,
liver, uterus, ovary and heart. Lower levels seen in brain and
intestine. Extremely low in calvaria, mammary glands and testis.
-!- DEVELOPMENTAL STAGE: Expressed predominantly in neonatal tissues,
                                                                                                                                                                                                                                                                                                                                                                                            1
                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DEVELOPMENTAL STAGE: Expressed predominantly in neonatal tissues at lower levels in adult.
-!- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, molear accumulation of beta-catenin and activation of full with target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated transact. Activation by Wnt8 induces expression of beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99324245; PubMed=10395542;
Sheldahl L.C., Park M., Malbon C.C., Moon R.T.;
"Protein kinase C is differentially stimulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homologs in a G-protein-dependent manner.";
Curr. Biol. 9:695-698(1999).
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Q08463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vuong V., Bambino T., Liu M.Y.C., Arnaud Nissenson R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Sprague-Dawley; TISSUE-Osteosarcoma; MEDLINE=93094228; PubMed=1334084; Chan S.D.H., Karpf D.B., Fowlkes M.E., Hook
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation updat
Frizzled 1 precursor (Frizzled-1) (Fz-1) (r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41,
28-FEB-2003 (Rel. 41,
10-OCT-2003 (Rel. 42,
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                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 frizzled (FZ) domain.
                                                                                                                                                                                                                                                                                                                                                                               similarity). SIMILARITY: Belongs to the Fz/Smo G-protein coupled receptor \overline{\mbox{SIMILARITY}}
                                                                                                                                                                                                                                                                                                                                                                                                                         the Wnt/beta-catenin signaling pathway (By similarity) DOMAIN: The FZ domain is involved in binding with Wnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              target genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chem. 267:25202-25207(1992).
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STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

MEDLINE-97313267; PubMed=9169871;

Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge m.,

Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,

Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,

Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,

Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,

Mueller-Auer S., Mentwich U., Obermaier B., Piravandi E., Pohl T.M.,

Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,

Charfe M., Scharens B., Scholler P., Schwager C., Schwarz S.,

Charfe M., Scharens B., Scholler P., Schwager C., Schwarz S.,
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Dancis A., Roman D.G., Anderson G.J., Hinne
"Ferric reductase of Saccharomyces cerevisi
characterization, role in iron uptake, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast)
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                             Proc. Natl. [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=F113;
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G-protein coupled receptor; Transmembrane; tein; Wnt signaling pathway; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetaceae;
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EMBL; U14913; AAB67424.1;
PIR; S30075; S30075.
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MEDLINE=93057491; PubMed=1431884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005886; C:plasma membrane; IDA.
GO:0000293; F:ferric-chelate reductase activity; IDA.
GO:0015677; F:copper ion import; IDA.
GO:0006826; F:iron ion transport; IDA.
erPro; IPR002916; Ferric reduct.
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CATALYTIC ACTIVITY: NADH + 2 Fe(3+) = NAD(+) + 2
COPACTOR: FAD (Probable).

SUBCELLULAR LOCATION: Integral membrane protein.
INDICTION: BY IRON DEPRIVATION. REPRESSED BY IRO
SIMILARITY: Belongs to the FRE / CVBB family.
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FUNCTION: Reductase activity that acts on ferric iron Guerac FUNCTION: Reductase activity that acts on ferric iron Gray external to the cell. Plays a role in iron uptake. May participate in the transport of electrons from cytoplasm to extracellular substrate (ferric ion) via FAD and heme extracellular substrate (ferric ion) via FAD and heme
144 RSQWCAWGLVFFWVAVL 160
                                                                              Similarity
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ERP1 YEAST
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MEDLINE=99287733; PubMed=10359606;
Marzioch M., Henthorn D.C., Herrmann J.M.,
Bergeron J.J., Solari R.C., Rowley A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4932;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Putative protein SH_(SH-4).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus,
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Adelman J.P., Bond
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106 AA;
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FUNCTION: May be involved with the regulation of GNRH gene expression. It is not known if this protein is transcribed
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mammalian genes transcribed from
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DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 21, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
DT 28-FEB-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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GO; GO:0030138; C:CODFII-coated vesicle; GO; GO:0016888; P:ER to Golgi transport; InterPro; IPR000348; Emp24_gp25L_p24.
InterPro; IPR009338; GOLD.
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-i- SUBUNIT: Associates with EMP24, ERV25 ar
-i- SUBCELLULAR LOCATION: Type I membrane pr
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SIMILARITY: Belongs to the
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  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sturr M.G., Krulwich T.A., Hicks D.B.;
"Purification of a cytochrome bd terminal oxidase encoded by Escherichia coli app locus from a delta cyo delta cyd strain complemented by genes from Bacillus firmus OF4.";

U. Bacteriol. 178:1742-1749(1996).

I- PUNCTION: CYTOCHRONE OXIDASE SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01654; Bac_Ubq_Cox; 1.
Oxidoreductase; Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D90735; BAA35743.1; -. PIR; S17958; S17958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- INDUCTION: IS INDUCED WHEN BACTERIAL CULTURES I
PHASE; ITS SYNTHESIS IS TRIGGERED BY PHOSPHATE
SHIFT FROM AEROBIC TO ANAEROBIC CONDITIONS.
-!- PIM: The N-terminus is blocked.
-!- SIMILARITY: STRONG, TO E.COLI CYDA.
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Respiratory chain; terminal step.
-!- SUBUNIT: Heterodimer of subunits I and II (Probable).
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage manner. 3:137-155(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                         TRANSMEM
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    ME.
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POTENTIAL.
IRON (HEME AXIAL LIGAND)
2D2FBD43429D960D CRC64;
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              (POTENTIAL).
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E STARVATION OR A
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                  (BY SIMILARITY).
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Best Local
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                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                             EMBL; AB028128; BAA96291.1;
EMBL; AF312922; AAX28487.1;
EMBL; AF312923; AAK28486.1;
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                                                                                                   MIM;
                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Composed of three subunits; DPM1, Associated with DPM1 via its C-terminal do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate tumor invasion.";
Oncogene 20:2781-2790(2001).
-!- FUNCTION: Stabilizer subunit of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Manos E.J., Kim M.L., Kassis J., Chang P.Y., Wells A., "Dolichol-phosphate-mannose-3 (DPM3)/prostin-1 is a nophospholipase C-gamma regulated gene negatively associated processing the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Dolichol-phosphate mannosyltransferase subunit 3) (Dolichyl-phosphate beta-D-mannose synthase subunit 3) (Mannose-P-dolichol synthase subunit 3) (Mannose-P-dolichol synthase subunit 3) (Prostin 1)
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                                                                                                                           Genew;
                                                                                                                                                                                                                                                                 entities requires a license agreement
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-!- SIMILARITY: Belongs to the DPM3 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20296673; PubMed=10835346;
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IsoId=Q9P2X0-2; Sequence=VSP
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IsoId=Q9P2X0-1; Sequence=Displayed;
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  (See http://www.isb-sib.ch/announce/
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Best Local
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                                                                                                           DOMAIN
DOMAIN
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston K.,
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Component of the peroxisomal translocation machinery
with PEX14 and PEX17. Functions as a docking factor for the
                                                                                        SEQUENCE
                                                                                                                                                                                                                             PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003
28-FEB-2003
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Q19951;
15-DEC-1998
Local 5.
                                                                                                                                                                                               Peroxisome;
                                                                                                                                                                                                                                                                                           Pfam; PF04088; Peroxin-13_N; Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007223; Peroxin-13 N. InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                               WormPep; F32A5.6; CE28290.
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pauley A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable peroxisomal membrane protein PEX13 (Peroxin-13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F32A5.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
SIMILARITY: Contains 1 SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predominantly cytoplasmic PTS1 receptor similarity).
SUBCELLULAR LOCATION: Integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                       P00519;
                                                                                                                                                                                                                                                                                                                                                                                                                        U20864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŋ
                                                                                                                                                                                                            PS50002; SH3; 1.
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                                                                                      235
330 AA;
                                                                                                                              193
214
                                                                                                                                                                                      Transport; Protein transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92
        Conservative
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2 AA;
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213
330
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10080 MW;
                                                                                        35765 MW;
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                                             29.3%;
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      2;
                                                                SH3.
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                         Score 49.5;
Pred. No. 2
                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                       LUMENAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49.5;
Pred. No. 7.
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V -> L (IN REF. 2)
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C350B3696842A877 CRC64;
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    Mismatches
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                                             DB
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    11;
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-
                                                                                 CRC64;
                                      Length 330;
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RESULT 14
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AC P74055;
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30-MAY-2000
                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                 TIGRFAMS; TIGR00546; lnt; 1.
PROSITE; PS50263; CN_HYDROLASE;
                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00795; CN_hydrolase; TIGRFAMs; TIGR00546; lnt; 1.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- PATHWAY: Lipoproteins biosynthesis.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similar
-!- SIMILARITY: Belongs to the apolipoprotein N-acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apolipoprotein N-acyltransferase (EC 2.3.1.-)
LNT OR SLR0819.
                                                                                                                                                                                                                                                                                                                    Fransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 CN hydrolase domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Res. 3:109-136(1996)
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004563; Lnt.
InterPro; IPR003010; Ntlse/CNhydtse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Transfers the fatty acyl group
                                                                                                                                                                                                                                                                                                                                                                                                                       ; D90911; BAA18131.1;
$75570; $75570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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131 GTASWCGLETLWSHSILW-----WS 150
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                                                                                      Similarity
                                  GRASWC---
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                                                                                                                                           519
                                                                     Conservative
                                                                                                                                                          47
126
174
206
277
239
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(Rel. 39, Last sequence up)
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                  Acyltransferase;
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67
103
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                                 WALALLWLAVVPGWS
                                                                                                                                       58130 MW;
                                                                                    29.3%;
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                                                                Score 49.5; I
Pred. No. 35;
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                                                                                                                                                                                                                                                                                                           Transmembrane; Complete proteome
                                                                                                                                     W HYDROLASE.
A28C75F260EF8BA3 CRC64;
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synechocystis
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                                                                                                   Length 519;
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Kimura T.,

Okumura f
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X MEDLINE-22288257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Pillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Yullalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Pinterion M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

T "Generation and initial analysis of more than 15,000 full-length

L Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                              A Lonka L., Kyttaelae A., Ranta S., Jalanko A., Lehesjoki A.-E.;

"The neuronal ceroid lipofuscinosis CLN8 membrane protein is a

resident of the endoplasmic reticulum.";

L Hum. Mol. Genet. 9:1691-1697(2000)

-i- SUBCELULIAR LOCATION: Integral membrane protein. Endoplamic reticulum and ER-Golgi intermediate compartment (ERGIC).

-i- PTM: Does not seem to be N-glycosylated.

-i- DISEASE: Defects in CLN8 are a cause of progressive epilepsy with mental retardation (EPMR) [MIM:600143]; also known as neuronal ceroid lipofuscinosis type 8 and Northern epilepsy. EPMR is an autosomal recessive disorder characterized by normal early development, onset of generalized seizures between 5 and 10 years, and subsequent progressive mental retardation. Biochemically, the disease is characterized by the intracellular accumulation of hydrophobic material, mainly ATP synthase subunit C.

-i- SIMILARITY: Contains 1 TLC (TRAM/LAGI/CLN8) domain.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION, AND MUTAGENESIS OF 283-LYS-LYS-284
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The neuronal ceroid lipofuscinoses in human are associated with mutations in CLN8.";
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Lehesjoki A.-E.;
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Ranta S., Zhang Y., R
Sharp J., Wheeler R.,
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                 DATABASE: NAME=NCL CLN8; NOTE=Neural Ceroid Lipofuscinoses mutation
WWW="http://www.ucl.ac.uk/ncl/CLN8.html".
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Kusumi K., Mole S., Liu W., Soares M.B.,
iemi A., de la Chapelle A., Gilliam T.C.,
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SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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Matches 7
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EMBL; AF123758; AAF13116.1; --
EMBL; AF123759; AAF13117.1; --
EMBL; AF123750; AAF13118.1; --
EMBL; AF123761; AAF13119.1; --
EMBL; BC007725; AAH07725.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GC; GO:0005783; C:endoplasmic reticulum; TAS.GO; GO:0005793; C:ER-Golgi intermediate compa.GO; GO:0016021; C:integral to membrane; TAS.GO; GO:0007399; P:neurogenesis; TAS.GO; GO:00007399; P:neurogenesis; TAS.GO; GO:0007399; P:neurogenesis; TAS.GO
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SM00724; TLC; 1.
E; PS50922; TLC; 1.
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                                              AGAARGRASWCW 16
ADKARGQQNWCW 104
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 KK->RR: LOCALIZES TO THE GOLGI N -> S (IN REF. 2).
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R -> G (in EPMR).
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Search completed: June 8, 2004, 14:04:38 Job time: 1.25 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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169
1 MRRGAGAARGRASWCWALALLWLAVVPGWS 30
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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brucella	brucella	07vxu4 bordetella	bordetella	O88di6 pseudomonas	O8ud14 agrobacteri	anthomonas		OBZSBO PYTOBACULUM		082sx8 mitrosomona	xvlella f	TVIPIIA F	08vm97 alcalidenes	ritreoscill	xvlella f	orvza sat	09xea6 sorahim hic	Q9mia5 typhlonecte	sorahum b	OBlni9 orvza sativ	092529 hematitie	OB 9hk3 bradyrhi vob	chlan	xv]e]	Ogneh4 xvlella fac	0777	ralstonia	07xsv0 orvza sativ

ALIGNMENTS

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	EMBL; AE005121; AAG20487.1; PIR; C84390; C84390.	-:- SIMILARITY: WITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING- PROTEIN-DEPENDENT TRANSPORT SYSTEMS.		SYSTEM. PROBABLY RESPONSIBLE FOR THE TRANSLOCATION OF THE SUBSTRATE ACROSS THE MEMBRANE (BY STATE ACTION	-!- FUNCTION: PROBABLY PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT	lobacterium species NRC-1.";	Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;	, Spudich J.L., Jun	Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,	Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.	Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y A.	.D., Lasky S.R., Baliga N.S., Thorsson V Shroma	NG W.V., Kennedy S.P., Mahairas G.G. Bermist B. Dan M	SEQUENCE FROM N.A.		NCBI TaxID=64091;	Halobacteriaceae; Halobacterium.	Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).		m permease	BLrel. 24,	01-MAR-2001 (Trambirel 16, Created)		Q9HMT4 PRELIMINARY; PRT; 606 AA.	ULT 1 MT4

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C STRAIN-ATCC 3913 / NCPPB 528;

K MEDLINE-22022145; PubMed=12024217;

K da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Morneiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Quaggio R.B., Monreiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

A Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Formighteri E.F., Franco M.C., Greggio C.C., Gruber A.,

Formighteri E.F., Franco M.C., Greggio C.C., Gruber A.,

Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

A Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

B Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

A Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
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01-OCT-2002 (TrEMBLrel.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein XCC0380.
XCC0380.
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Q8PDF8;
01-OCT-2002
01-OCT-2002
01-MAR-2003
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Hypothetical protein; Complete proteome.

SEQUENCE 205 AA; 23048 MW; CCCID7CB8AF9A482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P., "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with differing "Comparison of the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes of two Xanthomonas pathogens with the genomes with the genomes of two Xanthomonas pathogens with the genomes with
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EMBL; AE012134; AAM39699.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            host specificities.
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InterPro; IPR000847; HTH Lysr.
Pfam; PF00528; BPD transp; 2.
PROSITE; PS00404; BPD TRANSP INN MEMBR; 1.
PROSITE; PS00044; HTH LYSR FAMILY; 1.
Transmembrane; Transport; Complete proteome.
SEQUENCE 606 AA; 63066 MW; 2E64B9A2029BA28C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003848; DUF218.
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                    RRGAGAARGRASWCWA-----LALLWLAVVPGW
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Last
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Pred. No. 0.92;
3; Mismatches 11;
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Pred. No. 2.1;
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    sequence update)
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Q82G94
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RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Faria J.B., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Setubal J.C., Kitajima J.P.,
RA Setubal J.C., Kitajima J.P.,
Nost specificities.",
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Best Local
                                                                                               STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; MEDLINB=21477403; PubMed=11572948; Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahash Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Os Kikuchi H., Shiba T., Sakaki Y., Hattori M.; "Genome sequence of an industrial microorganism Strept avermitilis; deducing the ability of producing seconda metabolites.";
                  STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165; MEDLINE=22608306; PubMed=12692562;
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InterPro; IRR003848; DUF218.
Pffam; P702698; DUF218; 1.
Gomplete proteome.
70724 MW; 62D3709290F3D458 CRC64;
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobact Streptomycineae; Streptomycetaceae; NCBI_TaxID=33903;
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
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01-JUN-2003
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              Streptomyces avermitilis.
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EMBL; AE011664; AAM35272.1; -.
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MEDLINE=22022145; PubMed=12024217;
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STRAIN=306 / ATCC
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ia; Gammaproteobacteria; Xanthomonadales;
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Last annotation updat
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Pred. No. 1.
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i da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., i Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T., Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A., Fornighieri E.F., Franco M.C., Greggio C.C., Gruber A., Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.S.N., Martinez-Rossi N.M., Markins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D., Trindade dos Santos M., Truffi D., Tsai S.M., White F.F., Setubal J.C., Kitajima J.P.,
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Best Local
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    Q8PA94;
01-OCT-2002
01-OCT-2002
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TIGRFAMs; TIGR01352;
Complete proteome.
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Nat. Biotechnol. 21:526-531(2003).

EMBL; AP005037; BAC71716.1; -

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete proteome.

63428 MW; D8DC5F23BB49A321
                                                               Q8PA94
                                                                                                                                                                                                                                                                                                                               SEQUENCE
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EMBL; AE011797; AAM36519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Comparison of the genomes of two Xanthomonas host specificities.";
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MEDLINE=22022145; PubMed=12024217;
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Kanthomonas axonopodis (pv. citri).
Yanthomonas axonopodis (pv. citri).
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01-OCT-2002
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01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                    AARGRASWCWALALLWLAVVPGW 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||::|
| RGAGSSRTKLYATKNLTELIGVYGSRYGGDKSSWSWAGGLIWLAPRARW 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGAGAAR---
                                                                                                                                                                                                                                                                                                                               198 AA;
  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori
                                                                                                                                                                                                                                               Conservative
                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                               21748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ξ,
                                                                                                                                                                                                                                                                34.9%;
                                                                                                                                                                                                                                                                                                                                                               TonB_C.
tonB_Cterm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.7%;
  22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Omura S.;
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••
                       Created)
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Last
    Last
                                                                                                                                                                                                                                                              Score 59; DB Pred. No. 6.1;
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Pred. No.
                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                           FB9DF173EDC52961 CRC64;
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  sequence update)
                                                                                                                                                                83
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annotation update)
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                                                               198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                               DB 16;
                                                               A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
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                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogens with
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••
                                                                                                                                                                                                                                                                               Length 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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Best Local (
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=RB50 / ATCC BAA-588;
                                                                                                                                                                                                                                                                                                                                                           Bordetella bronchiseptica
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMI
01-OCT-2003 (TrEMI
Putative membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7WFK8;
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q7WFK8
                                                                                                                                                                                                                                                                                                                                        Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR006260; TonB_C.
TIGRFAMs; TIGR01352; tonB_Cterm; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 417:459-463(2002).
EMBL; AE012260; AAM40887.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Comparison of the genomes host specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 33913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GASPWLWATVLAVLVVVPSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRASWCWALALLWLAVVPGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                          Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                      protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.9%;
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25,
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Pred. No. 6.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304
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XX MEDILINE-22827954; PubMed=12910271;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Pellwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Fellwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT "Dordetella parapertussis and Bordetella bronchiseptica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RX MEDLINE=2022145; PubMed=1204217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Cicarelli R.M.B., Coutinho L.L., Craino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Formis B.C., Machado M.A., Madeira R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M. B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Moreira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Pereira H.A., Rossi A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Alcaligenes bronchisepticus).
Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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EMBL; BX640450; CAE
Complete proteome.
SEQUENCE 304 AA;
                                                                                                                             Q92VB2;
01-DEC-2001
01-DEC-2001
01-OCT-2003
                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical membrane protein SMb21292.
RB0796 OR SMB21292.
Rhizobium mellioti (Sinorhizobium mellioti).
Plasmid pSymB (megaplasmid 2).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Rhizobiaceae, Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N., Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L., Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K., Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C., Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Unwin L., Whitehead S., Barrell B.G., Maskell D.J.; "Comparative analysis of the genome sequences of Bordetella pertussis, Bordetella parapertussis and Bordetella bronchiseptica."; "Mat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
MEDLINE=22827954; PubMed=129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q7W451;
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
 SEQUENCE FROM N.A.
                                                                                                                                                                                       Q92VB2
                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome. SEQUENCE 304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; E
Alcaligenaceae; Bordetella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7W451
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                                                                                                                                                                                                                    φ
                                                                                                                                                                                                                                                                                                                                         Local
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les 15; Conserv
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; BX640450; CAE34627.1; -.
                                                                                                                                                                                                                                                                  182
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                                                                                                                                                                                                                                                                                                                                                                                                             BX640434; CAE39102.1; -.
                                                                                                                                                                                                                                                                                                                        l Similarity
                                                                                                                                                                                                                                                                                           4 GAGAARGRASW---CWAL-----ALLWLAVVPGW 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GAGAARGRASW---CWAL-----ALLWLAVVPGW 29
                                                                                                                                                                                                                                                              GARASRTLGGWRTICWALVVSVPALLPAVLWLAHDAAW 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parapertussis.
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                                                                                                                                                                                                                                                                                                                                                                                  304 AA;
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12910271;
                                                                                                                                                                                                                                                                                                                                                                                31640 MW;
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Pred. No. 9;
2; Mismatches
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Last annotation update)
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Pred. No. 9;
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RESULT 10
Q8CEK
ID Q8CEK
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DT 01-MA
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GN 93301
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DR EMBL;
DR MGD;
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SQU SEQUE
   RESULT 11
Q8G419
ID Q8G41
AC Q8G41
DT 01-MADT 01-MADT 01-MADT 01-MADT 01-MADDT 01-MA
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Best Local S
Matches 10
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Best Local
                                                           Q8G419;
Q8G419;
01-MAR-2003
01-MAR-2003
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STRAIN=C57BL/6J; TISSUE=Diencephalon;
MEDLINE=22354603; PubMed=12466051;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8CEK6;
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GO; GO:0005489; F:electron transporter activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IPR000345; Cytc. heme_BS.
PROSITE; PS00199; CYTOCHROME_C; 1.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 412 AA; 46126 MW; 8088BBE0C66FB838 CRC64;
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Finan T.M., Weidner S., Wong K., Buhrmester
Vorhoelter F.J., Hernandez-Lucas I., Becker
Golding B., Puehler A.;
Hypothetical BL1576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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01-MAR-2003
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9330132005RIK.
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NON_TER 1
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Pred. No. 12;
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Cowie
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01-JUN-2003
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                                                                                                          Q84X72
Q84X72;
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamot Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium
                CR066 protein.
Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 9:123-130(2002).
EMBL; AP005376; BAC09810.1; -.
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01-MAR-2003 (TrEMBLrel.
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T1r2258 protein.
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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Schell M.A., Karmirantzou M., Snel B., Vilanova D., E
Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley
Pridmore R.D., Arigoni F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to the human gastrointestinal tract.";
Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prissi G., Zwahlen M.-C., Desiere r., BOIK r., DELICY RI.,
Pridmore R.D., Arigoni F.;
"The genome sequence of Bifidobacterium longum reflects its adaptation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bifidobacterium longum.
Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
Bifidobacteriaceae; Bifidobacterium.
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12; Conserv
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226 AA;
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   Viridiplantae;
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                                                      (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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343 AA; 37507 MW; 8AE35FF32D22E059 CRC64;
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Chlorophyta; Chlorophyceae;
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Last sequence update)
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Pred. No. 1
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   Volvocales;
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RESULT
Q88SV3
ID Q8
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Best Local :
          Q88SV3;
01-JUN-2003
01-JUN-2003
01-QCT-2003
                                                                                                                                                                                                                                                                                                            MEDLINB-21128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Whogall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Buthoy S., Feltwell T., Fraser A., Hamlin N.
Holroyd S., Hornsby T., Jagels K., Lacroix C., MacLean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
  Cardiolipin
                                                           Q88SV3
                                                                                                                                                                                                                                                       "Massive gene decay in the leprosy Mature 409:1007-1011(2001).
EMBL; AL023635; CAA19188.1; -.
EMBL; AL583923; CAC30619.1; -.
                                                                                                                                                                                                                                   PIR; T44701; T44701.
Leproma; ML1666; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
Bacteria; Actinobacteria;
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01-JUN-2003
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Dutcher S.K.;
                                                                                                                                                                                                                                                                                                         Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Finished genomic sequence
Submitted (DEC-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           069464
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214 AA;
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(TrEMBLrel. 24, Created)
(TREMBLrel. 24, Last sequence update)
(TREMBLrel. 25, Last annotation update)
synthetase 2 (EC 2.7.8.-).
                                                                                                                                                                 Conservative
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                                                          PRELIMINARY;
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41.7%;
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Pred. No.
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Last annotation update)
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                                                                                                                   198
                                                                                                                                                                                                                                                                                            bacillus.";
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                                                          485 AA
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Schoolilus plantarum.

C. Bacteria; Pirmicutes; Lactobacillales; Lactobacillaceae;
C. Lactobacillus.
X. NCBI_TAXID=1590;
W. [1] __TAXID=1590;
W. REDILINE=22480296; PubMed=12566566;
X. MEDILINE=22480296; PubMed=12566566;
X. MIDILINE=22480296; PubMed=12566566;
X. MEDILINE=22480296; PubMed=12566566;
X. MIDILINE=22480296; PubMed=1256656;
X. MIDILINE=22480296; PubMed=125666;
X. MIDILINE=22480296; PubMed=125666; PubMed=125666;
X. MIDILINE=22480296; PubMed=125666; PubMed=125666; PubMed=125666; PubMed=1256666; PubMed=125666; PubMed=125666; PubMed=125666; PubMed=125666; PubMed
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Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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!rfect score:
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length: 2000000000
  BLOSUM62
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1758
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1: geneseqp1980s:*
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Listing first 45 sv
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                                     geneseqp2000s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sult No.

This invention describes the isolation of a novel human secreted protein, zsig46 encoded by a gene on chromosome 13 which is mainly expressed in the thyroid. This product can be used to study secretion of proteins from cells and also to treat or prevent deficient expression of zsig46, which may be associated with thyroid diseases (e.g. hypothyroidism, Graves' disease, thyrotoxicosis, thyroid cancer etc.) or with diseases that involve genes in the same region of chromosome 13 (e.g. Hirschsprung's disease, neuronal ceroid-lipofucinosis, Wilson disease and Reiger

Claim 3; Page 90-91; 101pp; English.

syndrome).

Antibodies

and

other binding

proteins,

are used as

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83	83	83.5	83.5	83.5	83.5	83.5	84.5	86	86	86.5	87	88	88	88.5	88.5	88.5	. 89	89.5	89.5
4.7	4.7	4.7	4.7	4.7	4.7	4.7	8	4.9	4.9	4.9	4.9	5.0	5.0	5.0	5.0	5.0	5.1	5.1	5.1
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AAW34563	ABB07927	AAE07981	AAE07983	AAW06592	ABU50828	AAB52581	AAR37508	ABU32653	ABB49050	ABB92540	AAB34827	ABU31122	ABU32174	AAM41004	AAM39218	ADD14088	ABB60986	ABG70004	AAW41856
Aaw34563	Abb07927	Aae07981	Aae07983	Aaw06592	Abu50828	Aab52581	Aar37508	Abu32653	Abb49050	Abb92540	Aab34827	Abu31122	Abu32174	Aam41004	Aam39218	Add14088	Abb60986	Abg70004	Aaw41856
	T. mariti	Attenuate	Dengue vi		Helicobac	Helicobac	Human DNA	Protein e	Listeria	Herbicida	Gene 17]	Protein e	Protein e	Human pol	Human pol	Human src	Drosophil	Larval vi	Ragweed p

ALIGNMENTS

RESULT 1 AAW92967

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New secreted polypeptide, zsig46, and its fragments, related fusion proteins - used for diagnosis and treatment of thyroid disorders or diseases involving genes on chromosome 13.
                                                                                                                                                                                                                                                                                                                                             Secreted protein; zsig46; human; chromosome 13; thyroid; disease; hypothyroidism; Graves' disease; thyrotoxicosis; thyroid cancer; Hirschsprung's disease; neuronal ceroid-lipofucinosis; Wilson disease
                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW92967 standard; protein; 346 AA.
                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                             AAW92967;
                                                                                                                                                                                    Sheppard PO,
                                                                                                                                                                                                                          24-JUL-1997;
                                                                                                                                                                                                                                              24-JUL-1998;
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                                                                                                                                                                                                                                                                                     WO9905275-A1
                                                                                                                                                                                                                                                                                                                                     Reiger syndrome;
                                                                                                                                                                                                                                                                                                                                                                                      Human zsig46 protein.
                                                                                                                                                                                                        (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                        1999-142930/12.
DB; AAX02855.
                                                                                                                                                                                                                                                                                                                             diagnostic.
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                                                                                                                                                                                     Gilbertson
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                                                                                                                                                                                                                                               98WO-US015431.
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Best Local S
Matches 316
19-MAR-1998;
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19-MAR-1998;
19-MAR-1998;
                                                                                                                                                                                                                                                                                                                             Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
                                                                                                                                                                                                                                                                                          cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
                                                                                                                                                              23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein encoded by gene 16 clone HMZAD77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY41323
                                                                                                                                                                                                   W09947540-AJ
                                                                                                                                                                                                                                                                                endocrine; metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reagents to detect zsig46 or cells expressing it, e.g. for assessing thyroid function to produce anti-idiotypic antibodies, for affinity purification of zsig46, to screen expression libraries, to neutralise zsig46 activity, and to deliver toxins, radioisotopes etc. for therapeutic or diagnostic purposes. Agonists of the product can be used to promote growth, differentiation and proliferation of specific cell types, e.g. for treating (extra)thyroid diseases or as additive to cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFBYWFLPMKFPFIKIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YEEIPLPIRNKTLSGL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLGLAIKREYYPEKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQG
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98US-0078563P.
98US-0078566P.
98US-0078573P.
98US-0078574P.
98US-0078576P.
                                                                                                                     99WO-US005804.
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                                                                                                                                                                                                                                                                            regulation; malabsorption; gastritis; neoplasm
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Pred. No. 3.6e-169;
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RESULT 3
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AAM93870 standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a secreted human protein encoded by the gene clome detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin Fc portion (e.g. AAZ24802) for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 95 novel genes and their fragments (nucleic acid sequences; AAZ24811-Z24907, amino acid sequences AAY41308-Y41404) which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also, pathological conditions can be diagnosed by determining the amount of the new polypucleotides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the 95 polynucleotides, based on which tissues they are most highly expressed in (see AAZ24811 for described uses)
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19-MAR-1998;
19-MAR-1998;
01-APR-1998;
01-APR-1998;
01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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N-PSDB; AAZ24826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human genes, useful cancers, neurological disorders,
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                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Endress G
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                                                                                                                                                                                                                                                                                                                                                                                                             347
                  YEEIPLPIRNKTLSGL 316
                                                                                                                                  ETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNK 240
                                                                         TLGLAIKREYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKIT
                                                                                                                 ETWFDSYDCSKFVLRTFNKLAEFGAEFKNIEXNYTXIFLYSGEPTYLGNETSVFGPTGNK
                                                                                                                                                                                             AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA 180
                                                                                                                                                                                                                                                          EFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQG
YEEIPLPIRNKTLSGL
                                                       TLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKIT
                                                                                                                                                                      AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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98US-0078579P.
98US-0078581P.
98US-0080312P.
98US-0080313P.
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ר RD,
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                                                                                                                                                                                                                                                                                                                                               Score 1747; DB 2;
Pred. No. 4.7e-168
0; Mismatches 2
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H, Ebner
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R, Lafleur DW,
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06-NOV-2001

(first entry)

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length numan cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota T, Ni
Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; SEQ ID NO 3978; 1380pp + Sequence Listing; English
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11-JAN-2000; 2000JP-00118774
02-MAY-2000; 2000JP-00183765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to primers for synthesising full length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         830 Primers useful for synthesizing full length cDNA clones in genetic manipulation.
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                                                                                                                                                                                                                                                                                                                        121 AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA 180
                                                                                                                                                                                                                                                                                                                                                                                                   103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                            YEEIPLPIRNKTLSGL 316
                                                                                                                  TLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFBYWFLPMKFPFIKIT 300
                                                                                                                                                                                                                             ETWEDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNK 240
                                                                                                                                                                                                                                                                                                                                                                                      EFKYGDLLGHLKIMHDAIGERSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQG 162
YEEIPLPIRNKTLSGL 358
                                                                                                                                                                                        ETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNK
                                                                                                                                                                                                                                                                                        AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVSGIPSRRHWPVPCKRFDFRPKPDPYCQAKYTFCPTGSPIPVMEGDDDTEVFRLQAPVW 102
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Pred. No. 9.9e-168;
0; Mismatches 2;
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K, Kojima
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S, Otsuki
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L T, Koga
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                                                                                                                                                                       Matches 163;
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format discretive form without first the carry to the cervical cancer.
                                                                                                                                                                                                                               Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US000670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM19604 standard; protein; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #6038 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM19604;
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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULAR DYNAMICS INC
                                                                                                                              AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
             IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 316
                                                                               YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV 273
                                                                                                                                                                                                                                                         from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                               AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 24430; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel
                                                                                                                                                                      50.4%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000US-0180312P.; 2000US-0207456P.; 2000US-00608408.; 2000US-00632366.; 2000US-0234687P.; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                      0,
                                                                                                                                                                                Score 886; DB 4; Pred. No. 2.8e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR
                                                                                                                                                                      Mismatches
                                                                                                                                                                      0;
                                                                                                                                                                                               Length 163;
                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               for analyzing
                                                                                                                                                                    Gaps
                                                                                                             60
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BB39239

D ABB3

X ABB3

X ABB3

X ABB3

X ABB3

X Peppl

X Peppl

X Home

X Claif

X Huma

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                                                                                                                                  ESULT 6
AM32740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
17-OCT-2001
                                                    AAM32740;
                                                                                                      AAM32740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2002
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                                                                                                                                                                                                                                                                                             274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLKTFNKLAEFGAEFKNIETN
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                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                 YRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
                                                                                                                                                                                                                                                                    IVHKQFYLFYNFEYWFLPMKFPFIKITYEBIPLPIRNKTLSGL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                      IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 31874; 639pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at
                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
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                                                                                                      163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 886; DB 4;
Pred. No. 2.8e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       foetal liver single exon probe
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                                                                                                                                                                                                                                         163
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RESULT 7
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AC ABB2
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Best Local S
Matches 163
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02345359.
04-OCT-2000; 2000GB-00024263.
         Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                            Protein #6079
                                                                                     23-JAN-2002
                                                                                                              ABB24080;
                                                                                                                                    ABB24080
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 33009; 654pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide #6777 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SG,
                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                     163;
                                                                                                                                                                                                                                                                                                                                                                                                                              genetic disorders
                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                      163
                                                                                                                                      standard;
                                                                                                                                                                                                                     IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                                                                                                                                                                                                                                                 AKWVKQDNETGIYYETWNVXASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                   YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
                                                                                                                                                                                                                                                                    YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
                                                                                                                                                                                                                                                                                                   AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                   IVHKQFYLFYNFEYWFLPMKFPFIKITYBEIPLPIRNKTLSGL
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                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                    (first entry)
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                                                           encoded by probe
                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                               50.4%; 50.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                                                                                      163
                                                                                                                                                                                                                                                                                                                                                   Score 886; DB 4;
; Pred. No. 2.8e-81;
0; Mismatches 0;
                                                           for measuring heart cell gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes
                                                                                                                                                                                                                                                                                                                                                                          Length 163;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                  163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for analyzing
                                                                                                                                                                                                                                                                                                                                                 0;
                                                           expression
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Homo sapiens

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                        Human; bone marrow expressed exon; gene expression analysis; probe
                                                                        Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measuring human gene expression in a sample derived from human heart (se. ABA21535-ABA41305). The present sequence is a protein encoded by one suci probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays.
  microarray; cancer;
                                                                                                                                    06-NOV-2001
                                                                                                                                                                                       AAM72492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                       AAM72492 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200157274-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                         274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRPYYPFKPHLPTKEFLLSLLQIFDAV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN 213
                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                               IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 316
                                                                                                                                                                                                                                                                                                                                                              IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKWVKQDNETGI YYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 25850; 530pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                              (first entry)
                                                                                                                                                                                                                                  protein;
leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 886; DB 4; Pred. No. 2.8e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart disease. Note: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Homo sapiens

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RESULT 9
AAMS 9901
ID AAMS
XX AAMS
AC AAMS
AC AAMS
XX Huma
XX Huma
XX Huma
XX Huma
XX Homc
XX Homc
XX WO20
XX WO20
XX S9-J
XX 30-J
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
             30-JAN-2001; 2001WO-US000667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                   WO200157275-A2
                                                                                                Homo sapiens.
                                                                                                                            Alzheimer's disease; multiple
                                                                                                                                         Human; brain expressed exon;
                                                                                                                                                                Human brain expressed single exon probe encoded protein SEQ ID NO: 32006.
                                                                                                                                                                                                05-NOV-2001
                                                                                                                                                                                                                            AAM59901;
                                                                                                                                                                                                                                                   AAM59901 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 32798; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157276-A2
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                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                       274
                                                                                                                                                                                                                                                                                                                                                                                                           214
                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SG,
                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                       Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                         IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 316
                                                                                                                                                                                                                                                                                                                         IVHKQFYLFYNFEYWFLPMKFDFIKITYEEIPLPIRNKTLSGL
                                                                                                                                                                                                                                                                                                                                                                              YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
                                                                                                                                                                                                                                                                                                                                                                                                       YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV 273
                                                                                                                                                                                                                                                                                                                                                                                                                                     AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.4%; Score 886; DB 4; 100.0%; Pred. No. 2.8e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                                                                     163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                      gene expression
                                                                                                                            sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                         sion analysis; probe; microarray;
schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                        163
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60 213 0

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ESULT 10
BG54183
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Matches
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26-WAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359P.
04-CCT-2000; 2000CB-0204263.
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                           Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                    Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one o the probes of the invention
                                                                                         30-JAN-2001;
                                                                                                                   09-AUG-2001.
                                                                                                                                            WO200157273-A2
                                                                                                                                                                                                                                                               25-FEB-2003
                                                                                                                                                                                                                                                                                                                 ABG54183 standard; peptide; 163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-483446/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention provides a number of single exon nucleic acid
                                                                                                                                                                     sapiens.
                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                             274
                                                                                                                                                                                                                                                                                                                                                                                                                                                              214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 AKWYKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163;
                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                 IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL
                                                                                                                                                                                                                                                                                                                                                                                                  IVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPIRNKTLSGL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                   YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                        2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO 32006; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DK,
                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                    SEQ ID No 32831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 886; DB 4;
Pred. No. 2.8e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for analyzing gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         samples,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                            273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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15-NOV-2001

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RESULT 11
ABG42312
ID ABG42
XX ABG42
AC ABG42
XX IP-AU
XX Human
XX Human
XX Human
XX Human
XX Chror
KW Chror
KW tuber
KW tuber
KW Eamil
KW tuber
KW Eamil
XX Pullmc
KW pulmc
K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             뭥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                    Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                   Human; single exon probe; asthma; lung cancer; COPD; IID; chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABG42312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000; 2000GB-00024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome-derived single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 886; DB 4; ]
Pred. No. 2.8e-81;
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Best Local Similarity
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung derived mRNA and for the study of lung diseases such as asthma, lung
                                                                                                                                                                                                                                                                                                                                                                                cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (IID), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the
                                                                                                                                                                                                                                                                                                                      present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spatially-addressable
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                                                                                                                                                                                                                                                         Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complements or the 12387 open reading frames derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid probes for measuring gene expression in a sample derived
from human lung comprising single exon nucleic acid probes having one
12614 nucleic acid sequences mentioned in the specification, or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a spatially-addressable set of single exon
                                                                                                                                                                        163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
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                        YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
                                                                                                              AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
                                                                                     AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
  YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV
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; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
                                                                                                                                                                        Conservative
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                                                                                                                                                                                          Score 886; DB 5;
Pred. No. 2.8e-81;
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                                                                                                                                                                        Mismatches
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treating, prognosing on preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus crythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders (e.g., anaemia) cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which
                                                                                                                                                                                                                                                                                                                               The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABP54131-ABP56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; cardiovascular disorder; respiratory disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ov cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gastrointestinal disorder; urinary system disorder; drug screening;
gene therapy; chromosome mapping; forensic analysis;
antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 4034; 2922pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                         modulate ovarian antigen
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    for
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  therapy,
                      expression or activity. The polynucleotides may
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  mapping,
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RESULT 13
ABB60074
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         printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published pct sequences
                                                                             insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB772072). The sequence data for this patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form part of the patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form patent did not form pate
                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 7014; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
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The invention describes a complex of protein-protein interactions in Helicobacter pylori selected from 421 complexes given in the specification. The complex of protein-protein interactions are useful for screening for agents which modulate the interaction of proteins. Modulating compounds which binds to a targeted bacterial protein may be used for treating or preventing ulcers in a human or animal. This is the amino acid sequence of a selected interacting domain (SID), identified via protein-protein interactions. Note: Where the patent number printed
                                                                                                                                                                                                                                                                                                                            New complexes of protein-protein interactions in Helicobacter pylori, useful for identifying modulating compounds for treating or preventir
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Pred. No. 21;
49; Mismatches
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
Claim 25; SEQ ID NO 58749; 1766pp; English.
                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                      N-PSDB; ACA34695.
                                                                                                                                      WPI; 2003-029926/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #16352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2003
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                                                                                                                                                                                                                                        (ELIT-)
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                                                                                                                                                                           Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKFVLRTENKLAEFGAEFKNIET---NYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAI 246
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tive 28;
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                                                                                                                                                                           Haselbeck R, Yamamoto R,
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Forsyth
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                                                                                                                                                                           Zyskind JW;
Xu HH;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational arms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the properties of the activity of a gene in an operon required for the activity of a gene in an operon required for the activity of a gene in an operon required for the activity of a gene in an operon required for the activity of a gene in an operon required for the activity of a gene in an operon required for the activity of the gene in an operon required for the activity of the gene in an operon required for the activity of the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the gene in an operon required for the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhin K. pneumoniae or P. aeruginosa. The present sequence is encoded by the target prokaryotic essential genes. Note: The sequence data for patent did not form part of the printed specification, but was obtain electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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FPFI-KITYEEIPLPIRNKTLSG 315
                                                                           SDFYDWTGGGYDFTGN-
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                                                                                                                                                                                                               LNFVGATEINIA--GATFKNLKTTSQNSYMTFMALGD-
                                                                                                                                                                                                                                                                        SKFVLRTFNKLAEFGAEFKNIET---NYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAI 246
                                                                                                                                                                                                                                                                                                                                                               KTGYITGTFTADRVYITGNMM---
                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTLVQVAT-----ISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTQTYGGKNSALVF-----NATTP-----
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                                                                       ---GVFDSVNFNKAYYKFQGTENSYNFKNTNFLAGN 683
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Search completed: June 8, 2004, 14:03:58
Job time: 84.8278 secs

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706

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression

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ximum DB
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Maximum Match 100%
Listing first 45 summaries
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mrfect score;
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match Length
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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1758
1 RVSGIPSRRHWPVPYKRFDF.....IKITYEEIPLPIRNKTLSGL 316
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                                                               GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
   DB
US-09-108-006C-1
US-09-157-021-31
US-09-157-021-31
US-09-156-842-31
US-09-1514-31
US-09-1514-31
US-09-489-039A-715-0
US-09-134-079-24
US-09-079-030-217
US-09-079-030-1
US-09-079-030-1
US-09-489-039A-7854
US-09-489-039A-11849
US-09-489-039A-12461
US-09-489-039A-12461
US-09-489-039A-12461
US-09-489-039A-12461
US-09-489-039A-1256
US-09-134-000C-6185
US-09-134-000C-6185
US-09-134-001C-5259
US-09-134-001C-5259
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US-08-781-802-4
US-08-781-802-4
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Sequence 24, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 1, Appli
Sequence 19, Appli
Sequence 1944, Appli
Sequence 11849, A
Sequence 11849, A
Sequence 12461, Appli
Sequence 12461, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
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Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 1503, Appl
Sequence 3624, Ap
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US-09-108-006C-1
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75.5	75.5	75.5	75.5	75.5	75.5	76	76	77	77	77	77	77	77	77	77	77	77
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Sequence 2, Appli	ν,	Sequence 2, Appli	•	Sequence 18, Appl	Sequence 14149, A	Sequence 2, Appli	Sequence 5806, Ap	Sequence 4897, Ap	Sequence 6507, Ap	Sequence 32, Appl	Sequence 24, Appl	Sequence 22, Appl	Sequence 20, Appl	14,	Sequence 6, Appli	Sequence 4, Appli	Sequence 6, Appli

ALIGNMENTS

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Sequence 1, Application US/09108006C Patent No. 6524613
GENERAL INFORMATION:
                                                             TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
                                                                                                     NAME: Friebel, Thomas
REGISTRATION NUMBER: 29258
REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRAETSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 18940
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bandyopadhyay, Paramita
Roy-Chowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steer,
                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/054,288
FILING DATE: 30-APR-1997
APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: PCT US 98/08834
FILING DATE: 30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/108,006C
FILING DATE: 30-Jun-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA
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                  LENGTH: 4563 amino acids
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amino acid
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                                   MOLECULE TYPE: IS-07-792-600-31
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IS-07-792-600-31
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Best Local :
 Query Match
                                                                                                                                            TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: STDU
TELECOMMUNICATION INFORMATION:
TELETHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: COPELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: COPELAND, WILLIAM C.
APPLICANT: WANG, TERESA S.-F.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC
                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                       TOPOLOGY:
                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                        FILING DATE: 19911115
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                       LENGTH:
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4118 ----GAIREIDDIDERFOKGASGTTGTYQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4013 MDEDDDFS-----KWNFYYSPQSSPDKKLTIFKTELRVRESDEETQIKVNWEEEAASG
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                                                                                    AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQEGQASFQGLKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPRFQFPGKPGIYTREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 Montgomery Street,
                                                                                                       1462 amino acids
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                                                    peptide
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 Score 88.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Suite 710
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US-09-157-021-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-157-021-31
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SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Design Assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 20.3%;
Matches 71; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                              Query Match 5.0%; Score 88.5; D Best Local Similarity 20.3%; Pred. No. 2.2; Matches 71; Conservative 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 31, Application US/09157021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: STDU-03484
CURRENT APPLICATION NUMBER: US/09/157,021A
CURRENT FILING DATE: 1998-09-18
EARLIER APPLICATION NUMBER: 07/792,600
EARLIER FILING DATE: 1991-11-15
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 1462
                                                                                                                                                                                                                                        243
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                                                                                                                                                                                                                                                                                                                   183 KKRSIGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAGDDVQVESTEEEQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 WDKES----EPAEEVKQEADSGKGTV----SYLGSFLPDVSCWDIDQEGDSSFSVQEVQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 KREDEREKPDPYCOAKYTECPTG-----SPIPVMEGD---DDIEV----FRL 55
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                                                                                                                                                                                          WCNQGAACFFEGIDDVHWKEN---GILVQVATISGNMFNQMAKW-VKQDNETGIYYETWN 171
                                                                                                                                                          WDKES----EPAEEVKQEADSGKGTV----SYLGSFLPDVSCWDIDQEGDSSFSVQEVQ 323
                                                                                                                                                                                                                                        ESGAMEFEDGDF---
                                                                                                                                                                                                                                                                             QAPVWEFKYGDLLGHLKIMHDAIGERSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPF 115
                                                                                                                                                                                                                                                                                                                                                         KREDERPKPDPYCQAKYTECPTG-----SPIPVMEGD---DDIEV----FRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRSIGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAGDDVQVESTEEEQ 242
  ERT-----LY----FLPREMKIDLNTGKETGTPISMKDVYEEFDEKIATKYKIMK----
                                 ETNYTRIFLYSGEPTYLGNETSVFGPTGNKT-LGLAIKRFYYPFKPHLPTKEFLLSLLQI 269
                                                                         VDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLFGKVWIESAETHVSCCVMVKNI
                                                                                                                VKASP---EKGAET-----WFDSYD---CSKFVLRTFNKLAEFGAE----FKNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WCNQGAACFFEGIDDVHWKEN---GTLVQVATISGNMFNQMAKW-VKQDNETGIYYETWN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56;
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6; Mismatches
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                                                                                                                                                                                                                                        ---DEPMEVEEV----
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FDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYE----EIPLPIRNKTLS

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CURRENT APPLICATION NUMBER: US/09/591,514
CURRENT FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: US/09/157,021
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 07/792,600
PRIOR FILING DATE: 1991-11-15
NUMBER OF SEO ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 31
                                                                                                                                                                                                                                                 Sequence 31, Application US/09591514
Patent No. 6670161
GENERAL INFORMATION:
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GENERAL INFORMATION:
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Patent No. 6103473
  SEQ ID
                                                                                                                                                                                                                                                                                                          -09-591-514-31
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ORGANISM: Homo
-09-156-842-31
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                                                                                                                                                                     APPLICANT: Copeland, William C.
APPLICANT: Wang, Teresa S. F.
TITLE OF INVENTION: Drug Design Assay
FILE REFERENCE: STDU-03484
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Pred. No. 2.2;
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LENGTH: 608
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27
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TYPE: PRT
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    388
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                                                                                                                                                                                                                                     103 TEPHLRPEMDAPF----WCNQGAAC--
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DAEDAAMNYRGFTFPIWGFLANTDISYDPOKIDAQTCMAWMDNYRAGISHQQQIRMFNQI
                                           D-----NETGIYYETW-----NVKASPEK-GAET---WFDSYDCS---KFVLRTFNKL 200
                                                                                          KAPWSMDGWRLDVVHMLGEGGGARNNLQHIAGITQAAKQAQPEAFVFGEHFGDARQWLQA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDKES-----EPAEEVKQEADSGKGTV----SYLGSFLPDVSCWDIDQEGDSSFSVQEVQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WCNQGAACFFEGIDDVHWKEN---GTLVQVATISGNMFNQMAKW-VKQDNETGIYYETWN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKRSIGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAGDDVQVESTEEEQ 242
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                                                                                                                                                                                                                                                                                                                                                                         5.0%; Score 88; DB 4 ilarity 20.9%; Pred. No. 0.64; Conservative 41; Mismatches
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                                                                                                                                           --NGTLVQVATIS-------GNMFNQMAKWVKQ 159
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                                                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 608;
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                                                                                                                                                                                                                                     ---FFEGIDDV--HWK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---DLEP-MAAKA 272
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8-09-134-078-24
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09134078 Patent No. 6368844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 3624
LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3624, Application US/09134000C Patent No. 6617156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CURRENT APPLICATION DATA:
                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                       APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: GLYCOSIDASE ENZYMES
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                  COUNTRY:
                                                                                                                                                                                            CITY: San Diego
                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNMFNQM----AKWVKQDNETGIYYE-----TWNVKASPEKGAETWFDSYDCSKFVLR 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNYTRRIGERTDLSKGYISQLERDLSSP----SMETEF-----SILEVLGVT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFYYPFKPHLPTKEFLLSLLQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFDK----NGEYKTFEPSLSETFIYVIDGSIRLTLGEATYIAKK----GQT---
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                                                                                                                                                                                                                 E: Gray Cary Ware & Freidenrich LLP 4365 Executive Drive, Suite 1600
                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.0%; Score 87.5; DB 21.6%; Pred. No. 0.11; tive 24; Mismatches
                                                                                                                                                                                                                                                                                       72
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RESULT 9
US-09-079-030-217
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 858/677-1456
TELEPAX: 858/677-1465
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 217, Application US/09079030 Patent No. 6635623 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogeveen, Ron C.
APPLICANT: MOORE, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein FRAGMENT TYPE: internal
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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FILING DATE: 10-OCT-
APPLICATION NUMBER:
FILING DATE: 06-DEC-
                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: P.
               CLASSIFICATION:
                                                   APPLICATION NUMBER: US/09/079,030
                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                             CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 FCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEW 93
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Y: USA
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                                                                                                                                                                                                                                                                                 White & Durkee
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                                                                                           Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDDAYEKDIGDWLVTRGDFPSVEE 245
                                                                                                                                                                                                                                                                                                                                          EUKARYOTIC CELLS
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Sequence 27, Applicati
Patent No. 6444644
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 217:
INFORMATION
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REGISTRATION NUMBER: P.43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
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          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998

CLASSIFICATION: CUTKNOWN-
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 117-268
REFERENCE/DOCKET NUMBER: 117-268
TELLEPHONE: 7038164000
TELLEPHONE: 7038164100
TELLEPAX: 7038164100
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TELEFAX: 512/474-7577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON & VANDERHYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BRUCKDORFER, KARL R
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: VA
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RESULT 11
US-09-079-030-1
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-180-422B-27
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                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently ucco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09079030 Patent No. 6635623
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
GEOVERA, Jr., Juan G.
APPLICANT: Hoogeveen, Ron C.
APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
                                                      TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MCMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SECULIAR SECULIAR SECULIAR ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE APPROVED White & Durkee
                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 512/418-3000
LENGTH: 455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 77210
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                                                                                                                 TELEPHONE:
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                                     4536 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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19.7%;
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Pred. No. 54;
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CURRENT APPLICATION NUMBER: US/09/254,352B
CURRENT FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/JP98/03039
PRIOR FILING DATE: 1999-07-06
PRIOR APPLICATION NUMBER: JP 10-155847
PRIOR APPLICATION NUMBER: JP 9-196478
PRIOR APPLICATION NUMBER: JP 9-196478
PRIOR APPLICATION NUMBER: JP 9-196478
PRIOR APPLICATION NUMBER: JP 9-196478
PRIOR FILING DATE: 1997-07-07
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
INVESTIGATION OF SEQ ID NO 19
INVESTIGATION OF SEQ ID NO 19
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OTHER INFORMATION: Description of Artificial Sequence:
'S-09-254-352B-19
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S-09-254-352B-19
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Matches
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APPLICANT: HAYASHIZAKI, Yoshihide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHOD OF DNA SEQUENCING FILE REFERENCE: 024705-080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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les 56; Conserv
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                                                                                                                                                                                 415 NFANHKAIWF-----PYNMDWRGRVYAVSMFGNDMTKGSLLTLAKGKPIGLDGFYWLK 467
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                                                                                                                                                                                                                                                                                                                      35 CPTGSPIPVMEGD-----DDIEVFRLQAPVWEFKYGDLLGHLKIM---
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                                           TWNVKASPEKGAETWFDSYDCS 190
                                                                                                                               -QGAACFFEGIDDVHWKENGTLVQVATISGNMFNQNAK---
                                                                                                                                                                                                                                                                        CPVGD-VPAIEREELPPRPDDIDTNEVARKAWRKEAAAVYRKDKAROSRRCRCEFMVAQA 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GAIRQIDDIDVRFQKAASGTTGTYQ------EWKDKAQNLYQELL
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
---HHGLNSYNCS
                                                                                                                                                                                                                                                                                                                                                                                         4.7%;
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19.7%; Pred. No.
ative 39; Mismatc
                                                                                                                                                                                                                                                                                                                                                               22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       Score 82; DB 4; Length 876; Pred. No. 5.5;
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535
                                                                                      -rikfieenegnilasaadplnntwatqqdspfafcfe
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                                                                                                                                                                                                                                                                                                                                                                      67;
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4640
LENGTH: 718
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-4640
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US-09-489-039A-7854
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7854
LENGTH: 741
                                                                 Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4640, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
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  194 DÉTCÓV--TYLALEAFLYEMGTKDAAGLDAYKLKLGLWSDIFVRNFNKINGAADQFNYGD
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                                     25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSQVQTDGR----WQKWDVTLASPSK-ATAWVGWAPDPWSLRVQSQQVFDLSDAAGNKLE
                                   DPYCOAKYTECPTGSPIPVMEGDD--DIEVERLOAPVW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGRTFGL 735
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                                                                             Conservative
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                                                                                              4.6%; Score 80.5; D
20.6%; Pred. No. 5.9;
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                                                                           41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---WCNQGAACFFEGIDDVHWKENGTLVQVATISGNMFNQM 153
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ib time : 25.5778 secs
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEHSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT ENLING DATE: 2709.200-01-27
PRIOR APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: US/00-01-27
PRIOR APPLICATION NUMBER: US/09/17,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11849
ENERGY # 511
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3-09-489-039A-11849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11849, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE; PRT
ORGANISM: Klebsiella pneumoniae
-09-489-039A-11849
                                                                                                                                                                                                                                                                                   166 YYETWN-VKASPEKGA-----ETWFDSYDCSKFVLRTENKLAEFGAEFKNIETNYTRIFL 219
                                                                                                                                                                                                                                                                                                                                            263 ----LENRKNVVYVRPVAAW-QSGAWSAAAAIESNLVNNAYGYQSQSGRWVDQSNRTGYG 317
                                                                                                                                                                                                                                                                                                                                                                                                   121 AACFFEGIDDY-----HWKENGTLVQVATISGNMFN-----QMAKWVKQDNETGI- 165
                                                                                                                                                                         220 YSGEPTYLGNETSVFGPTG 238
                                                                                                                                                                                                                                  318 LTMSWNTLKSDPQDGAVVNLSTALLDAADETDF-----SAGINALWHRVELGY----
                                                                                                                     366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 GYIYMMKEGRG-RSSSGGNLLFSKTVDNWYFEVNTLVEDGSSLF-----VDQNYHGNA- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 PLADMDGKMNLDDAAFFFGQQDDWKIKIGRFEAWDMFPLNQDTFIEYSGNTANDLYSDGY 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 GHLKIMHDAIGFRSTLTGK------NYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 PIPVMEGD---DDIEVFRLQAPVWEFK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IETNYTRIFLYSG-----EPTYLGNE-TSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNNGGTGSFGTSAGCRYYVEKRTRTDSKTATKTWDASGLSNAGVLRLSTR-
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                                                                                                                  --IYAHNKIDQFNMAG 379
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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itle:
erfect score:
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Published Applications AA:*

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6: /cgn2_6/ptcdata/2/pubpaa/US07_NEW_PUB.pep:*

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1758
1 RVSGIPSRRHWPVPYKREDF.....IKITYBEIPLPIRNKTLSGL 316
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

886 50.4 163 9 472 26 8 89 15	5.2 347 12	5 740 10	2 3 3 4 4 4 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	SCOTE 1758 1758 1758 1747 1747 1747 1747 1747 195.5 95.5 95.5 94.9 94.9
9 US-09-864-761-39378	15 US-10-264-049-4034 15 US-10-369-493-12714 16 US-10-408-765A-58 12 US-10-282-122A-58749 12 US-10-282-122A-55615	15 US-10-264-049-4034 15 US-10-369-493-12714 16 US-10-408-765A-58 12 US-10-282-122A-58749 12 US-10-282-122A-55615 12 US-10-424-599-662855	Query Query Match Length 100.0 346 100.0 346 99.4 347 99.4 347	Query Match Length D
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e 5705	equence 56	e 5672	equence 46266,	equence 156, A	e 156,	e 2336	equence 7666	equence	32,	Un		e N	2, Apr	Ų.	198,	Sequence 56258, A	6607	e 46548,	æ	æ	e 60577,	Sequence 12860, A	equence 590	6	e 2	e 3172, A	е 4, Арр	e 252265,	Sequence 128, App

ALIGNMENTS

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FILE REFERENCE: 97-38

CURRENT ELLING DATE: 1998-07-24

CURRENT FILING DATE: 1998-07-24

EARLIER APPLICATION NUMBER: 60/053,613

EARLIER FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 19

SOFTMARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

SEQ ID NO 2

LENGTH: 346
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                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Homo sapien US-09-122-383-2
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US-09-122-383-2
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                                                                                                                                                                                                                                                               Query Match 100.0%; Score 1758; DB 9; Best Local Similarity 100.0%; Pred. No. 5e-167; Matches 316; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED
TITLE OF INVENTION: CHROMOSOME 13
                         121 AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA 180
151 AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA 210
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                                                                                                              61 EFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLREEMDAPFWCNQG 120
                                                                                       EFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQG 150
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                               Sequence 126, Application US/10653595
Publication No. US20040048304A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 316; Conserv
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NUMBER OF SEQ ID NOS: 19

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 346

TYPE: PRT
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 09/122,383
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/053,613
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APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: SECRETED PROTEINS ENCODED BY HUMAN
TITLE OF INVENTION: CHROMOSOME 13
FILE REFERENCE: 97-38C1
 APPLICANT: Ruben et. TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapien
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95 Human
secreted proteins
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CURRENT APPLICATION NUMBER: US/10/653,595

CURRENT FILING DATE: 2003-09-03

PRIOR APPLICATION NUMBER: US 09/397945

PRIOR FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: PCT/US99/05804

PRIOR FILING DATE: 1999-03-18

PRIOR APPLICATION NUMBER: 60/078,566

PRIOR APPLICATION NUMBER: 60/078,576

PRIOR APPLICATION NUMBER: 60/078,576
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PRIOR APPLICATION NUMBER: 60/078,573
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,574
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 60/078,579
PRIOR FILING DATE: 1998-03-19
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Best Local (
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SEQ ID NO 126
LENGTH: 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/080,314
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080,312
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/078,578 PRIOR FILING DATE: 1998-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SITE
LOCATION: (246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE LOCATION: (242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                  RVSGIPSRRHWPVPYKRFDFRPKPDPYCQAXYTFCPTGSPIPVMEGDDDIEVFRLQAPVW
                                                                        TLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKIT
                                                                                                                                           ETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNK 240
                                                                                                                                                                                                      AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA 180
                                                                                                                                                                                                                                                                                  EFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQG
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YEEIPLPIRNKTLSGL 316
                                          TLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKIT
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Pred. No. 6.3e-166;
0; Mismatches 2;
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RESULT 4
US-09-397-945-126
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; Publication No. U

Application US/09397945 o. US20030065139A1

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SOFTWARE: Pai
SEQ ID NO 126
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PRIOR TILING DATE: 1999-03-18
PRIOR APPLICATION NUMBER: 60/078,566
PRIOR FILING DATE: 1998-03-19
PRIOR FILING DATE: 1998-03-19
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CURRENT FILING DATE: 1999-09-17
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TITLE OF INVENTION: 95 Human secreted proteir
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OTHER INFORMATION:
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NAME/KEY: SITE
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hes 314;
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FILING DATE: 1998-03-19
APPLICATION NUMBER: 60/078,579
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APPLICATION NUMBER: 60/078,581
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APPLICATION NUMBER: 60/080,312
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APPLICATION NUMBER: 60/078,577
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TLGLAIKREYYDEKDHLDTKEBLLSLLQIFDAVIVHKQFYLFYNFEYWFLDMKFDEIKIT
                                                                                                                                                                                                                                            EFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQG
                                                                        ETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNK
                                                                                                                                  AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA
                                                                                                                                                        AACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGA
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                                                 ETWFDSYDCSKFVLRTFNKLAEFGAEFKNIEXNYTXIFLYSGEPTYLGNETSVFGPTGNK
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LENGTH: 163
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
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  OTHER INFORMATION: MAR TO ACOO1226.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL =
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.
OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN HETAL LIVER, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN HETAL LIVER, SIGNAL = 5..
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00665
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SEQ ID NOS: 49117
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Chen, Wensheng
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RESULT 6
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Matches
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Matches
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NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 4034
LENGTH: 89
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Best Local Similarity
             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PA133P1
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CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
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NAME/KEY: MISC_FEATURE
LOCATION: (58)
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US/10/369,493
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                                                                                                                                                                                                                                                                                                                                      WFLPMKFPFIKITYEEIPLPIRNKTLSGL 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHLPTKEFLLSLLQIFDAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN
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98.9%;
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100.0%;
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Pred. No. 2.7e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 472; DB 15;
Pred. No. 2.9e-39;
0; Mismatches 1;
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; SEQ ID NO 12714
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-12714
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEILE REFERENCE: 66008.465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 836
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                                                                                                                           377
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                                                                                                                                                                                                                                                                                                                                      37 TGSPIPV-----MEGDDDIEVFRLQAPVWEFKYGDLLG---HLKIMHDAIGFRSTLTG
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  YYPEKPHLPTKEFLLSLLQIFDAVIVHKQFY---
                                                                                                                           LRRNLQDHAEWVYQ----GAIREIDDIDERFQKGASGTTGTYQ------- 415
                                                                                                                                                                                                          TQIKVNWEEEAASGLLT--SLKDNVP-----KATGVLYDYVNKYHWEHTGLTLREVSSK 376
                                                                                                                                                                                                                                                    KNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG-TLVQVATI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPLGGLGFAR--WAFEVEMQEKE----LGVFFDTVIV 185
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                                       EWKDKAQNLYQELLTQEGQASFQGLKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPRF 475
                                                                                   EFKNIETN-YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIK--
                                                                                                                                                                SGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGA 205
                                                                                                                                                                                                                                                                                              TSAPSPAVGTVGMDMDEDDDFS-----KWNFYYSPQSSPDKKLTIFKTELRVRESDEE 324
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20.5%; Pred. No. 2.7;
tive 39; Mismatches
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26.1%; Pred. No. 0.
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0.47;
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    --LFYNFEYWFLPMKFPFIK 298
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S-10-282-122A-58749
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 58749
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Publication No. US20040029129A1
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APPLICANT:
APPLICANT:
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TITLE OF I
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APPLICANT: Zamudio, Car
APPLICANT: Malone, Cher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 1238
                                                                                                                                                                                                                                                                                                                                                           Match 5.3%; Score 94; DB Local Similarity 23.6%; Pred. No. 6.4;
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APPLICATION NUMBER: 60/207,727
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APPLICATION NUMBER: 60/230,347
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APPLICATION NUMBER: 60/257,931
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635 SDFYDWTGGGYDFTGN-
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                                     KREY-----YPEKPHLPTKEFLLSLLQIEDAVIVHKQEYLE-----YNEEYW-FLPMK 293
                                                                                                                                                                  KTGYITGTFTADRVYITGNMM-----
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Malone, Cheryl
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moto, Robert
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                                                                                -GATFKNLKTTSQNSYMTFMALGD
                                                                                                                                                                                                                                                                                                                                     28;
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--GVFDSVNFNKAYYKFQGTENSYNFKNTNFLAGN 683
                                                                                                                                                                    ---TG----
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                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Enterobacter cloacae US-10-282-122A-55615
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PRIOR FILLING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Pater
SEQ ID NO 55615
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification of Essential Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/257,931 PRIOR FILING DATE: 2000-12-22
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PRIOR APPLICATION NUMBER: 60/242,578
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TYPE: PRT
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                                                                                                                                                                134 -----KENGTLVQVATIS------
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                                                                                                                                                                                                                                                     92 EWYE-----LFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDV--HW------
                                                                                                                                                                                                                                                                                             Similarity
56; Conserv
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----GAEFKNIETNYTRIFLYSGEP-TYLGNETSVFG---PTGNKTLGLAIKRFYYPFKP 255
                                        YRGFTFPLWGFLANTDISYDPNHIDAETCMAWMENYRAGLSHQQQLRMFNQLDSHDTARF 384
                                                                                                                        WRLDVVHMLGEAGRARNNLOHVAGITRSAKAAQPEAFVFGEHFGDARQWLQNDAEDAAMN 324
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Matches
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SEQ ID NO 262855
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                                                                APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Rober
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Wong, Hilary
APPLICANT: Cocker, Hilary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Flants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
                                                                                                                                                                               APPLICANT: Merberg, David APPLICANT: Treacy, Maurice
                                                                                                                                                                                                                          APPLICANT: Evans, Cheryl
          APPLICANT: Genetics Institute, Inc.
                                                      APPLICANT: Fechtel, Kim
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ORGANISM: Glycine max
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REFERENCE: GI 6075-83A
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Pred. No. 2;
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CURRENT FILING DATE: 199-08-13
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 160
LENGTH: 742
                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 160
LENGTH: 742
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Best Local Similarity
                                                                                              Best
                                                                                                              Query Match
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APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
FILE REFERENCE: 00766.000103.5
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                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-07-08
NUMBER OF SEQ ID NOS: 240
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ORGANISM: Homo
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                                                                                            Local
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325 GSAYQFHSWRVFVL-VCAFPSVFAIGALTTQPESPRFFLENGKHDEAWMVLKQVHDTNMR 383
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                                                                                            Similarity
                                  GKNYIMEWYELFQLGNCTFPH-----LRPEMDAP-FWCNQG----AACFFEGIDDVHWK 134
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LaVallie, Edward R.
Collins-Racie, Lisa F
Evans, Cheryl
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Steininger II, Robert J.
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                       Wong, Gordon G.
Clark, Hilary
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Treacy, Maurice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US20040038276A1
                                                                        5.2%; Score 91; DB 22.1%; Pred. No. 6.4; cive 39; Mismatches
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                                                                                                              DB 12; Length 742;
                                                                            105;
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                                                                            Gaps
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3SULT 15
3-09-870-759-128
                    Sequence 128, Application US/09870759
Patent No. US20020177551A1
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LENGTH: 742
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WAITHOCK, Dale E. TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROFILE REFERENCE: 660088.465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ghosh, Soumitre
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 5.2%; Score 91; DB 16; Length 742; I Similarity 22.1%; Pred. No. 6.4; 62; Conservative 39; Mismatches 105; Indels
                                                                                                                                                                                               TFINTVFYNTDLFEYKFVNSR--LINSTFLHNKEGCPLDV 587
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                                                                                                                                                                                                                                                 ---LFYN---FEYWELPMKFPFIKITY----EEIPLPI 308
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Search completed: June Job time : 65.9556 secs
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Best Local S
Matches 58
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
SEQ ID NO 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4563
                                                                                                                                                              4157
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                                                                               4217 CTMF-IREVGTVLSQVYSKVHNGSEILFSYFQDLVITLPFELRK 4259
                                                                                                                                                                                                       219 LYSGEPTYLGNETSVFGPTGNKTLGLAIK-----
                                                                                                                                                                                                                                                                                        160 DNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETN-YTRIF
                                                                                                                                                                                                                                                                                                                                                             101 NCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG-TLVQVATISGNMFNQMAKWVKQ
                                                                                                                       264 LSLLQIFDAVIVHKQFY-
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                   2004,
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                     14:11:58
                                                                                                                       --LFYNFEYWFLPMKFPFIK 298
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ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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aximum DB seq length: 2000000000
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erfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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87.5
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88.8
88
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Match
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 , Gapext 0.5
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1758
1 RVSGIPSRRHWPVPYKRFDF.....IKITYEEIPLPIRNKTLSGL 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       283366 seqs, 96191526 residues
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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BB
                          T37889
T27026
T49253
AF1352
JC6079
E72616
B59200
T51095
F71425
                                                                                                                       D85056
JC1486
T27404
T51094
DJHUAC
D69459
S27263
D71917
T41912
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T33904
A64596
T19604
T18995
F70316
T21702
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      hypothetical prote acid phosphatase (DNA-directed DNA p conserved hypothet synaptic vesicle p toxin-like outer m structural phospho probable nuclear p hypothetical prote purple acid phosphoprobable phosphoese chitin synthase (E hypothetical prote acid phosphatase (acid phosphatase (acid phosphatase (aphosphoesterase-re hypothetical prote cellulose 1,4-beta hypothetical prote hypothetical prote cellulose 1,4-beta hypothetical prote
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RESULT 1 A96816 A96816 F9K20.25 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear C;Date: 02-Mar-2001 #sequence_revision 02- C;Accession: A96816 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway ansen, N.F.; Hughes, B.; Huizar, L.		-	44 8	43	42	41	40	39	38					33	32	31	30	
mporte Arabid Mar-20 : A968 ; A.; ; Chun		81.5	1.5	82	82	82	82	82	82	82.5	82.5	82.5	82.5	83	83	83	83	
d] - A opsis 01 #se 16 Ecker, g, M.K		4.6	4.6	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	
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P C H	ALIGNMENTS	S19444	T39458	A43344	G70320	T03858	A36709	AH0842	T02640	B83914	A41043	S49349	AF3413	LPHUB	T33893	F70383	T27008	
naliana Ise-ear cress) Ion 02-Mar-2001 #text_change 31-Mar-2001 C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;		hypothetical prote	DNA binding protei	synaptic vesicle p	aldehyde dehydroge	hypothetical prote	alpha-amylase (EC	probable glycopori	hypothetical prote	beta-xylosidase (1	acetate-CoA ligase	cyprosin (EC 3.4.2	fosmidomycin resis	apolipoprotein B-1	hypothetical prote	organic solvent to	hypothetical prote	

UT 2	RESULT
284 YPGRPN 289	da
251 YPFKPH 256	γΩ
227 AFKIALITWSKWIDHNIDPSKTRVFYQGVSPVHLNGGEWGKPGKTCLGETVPVQGPS 283	DЪ
202 EFGAEFKNIETNYTRIFLYSGEPTYL-GNETSVFGPTGNKTLGLAIKRFY 250	8
172 GLILKLDSISRGNQWLGSDVAIFNTFHWWSHTGRAKTW-DYFQTGDKIVKEMNRME 226	DЬ
145ISGNMENQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLA 201	γQ
117 MWVSLSCMLHAAVPNAKYTFQLNKGLSTFTIPEYGI-SVNFLKNGFLVDLVSDKTR 171	Db
92 EWYELFQLGNCTFPHLRPEMDAPFWCNGGAACFFEGIDDVHWKENGTLVQVAT 144	80
80 YRWQPTGCDIPRFNGRDFLTRFKGKKILFVGDSLSNN 116	Дb
32 YTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTM 91	Ş
<pre>Query Match</pre>	Quei Best Matc
C;Genetics: A;Gene: F9K20.25 A;Map position: 1	A;Gene A;Map
A,Sdtatus: preliminary A,Molecule type: DNA A,Residues: 1-359 <sto> A,Cross_references: GB:AB005173; NID:g3834323; PIDN:AAC83039.1; GSPDB:GN00141</sto>	A;Stat A;Mole A;Resi A;Cros
A;Reference number: A86141; MUID:21016719; PMID:11130712	A;Refe A;Acce
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A. Title: Seminore and analysis of chromosome 1 of the plant arabidonsis	ker, l
o, M.; Rooney, T.; Rowley, D.; Sakano, H. thors: Salzberg. S.L.: Schwartz. J.R.: Shinn. P.: Southwick. A.M.: Sun. H.: Tallon. I	Rizzo, A:Aut]
A;Auchors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.c. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	C.A.;
Nature 408, 816-820, 2000	Natur

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: A64596
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3;Species: Helicobacter pylori
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submitted to the EMBL Data Library, February 1999
N; Description: The sequence of C. elegans cosmid
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                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE000575; GB:AE000511; NID:g2313730; PIDN:AAD07677.1; PID:g23137
                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown; translation not
A;Molecule type: DNA
A;Residues: 1-1238 <TOM>
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Best Local S
Matches 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: T33904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;Reference number: Z21437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nypothetical protein Y25ClA.7a - Caenorhabditis elegans
;Species: Caenorhabditis elegans
;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999;Accession: A64596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: CESP:Y25ClA.7a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:AF125459; PIDN:AAD12838.1; GSPDB:GN00020; CESP:Y25C1A.7a Experimental source: strain Bristol N2; clone Y25C1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
Residues: 1-362 <KAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: T33904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 APFWCNQGAACFFEGIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNV 172
                                                                                                                                                          513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7/1; 30/3; 79/3; 146/1; 231/1; 282/3; 323/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 IMHDAIGFRSTLTGKNYTMEWYELF------QLGNCTFPHLR------PEMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KASPEKGAE----TWFDSYDCS--KFVLRTFNKLAEFGAEFKNIETNYTRIFLYSGEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFDDSQSTTSTRKGNFFSFEYYQQFFDVETDQVIKRLLNSVIPTHRNYIQDFLQPIPDLW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FC-NLSHGFLINGNLKTGSFSEQKMNFYTSFITSASTLIFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YLGNETSVFGPTGNKTLGLAIKR---FYYPFKPHLPTKEFL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPFWVSV--
                                                                                                           ENGTLVQVAT----ISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AKIPENVTEISIFRAQFPKKNCKIIDFSMKKFQKINNLCESFKKKSD---
                     SKFVLRTFNKLAEFGAEFKNIET---NYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAI
                                                                 KTGYITGTFTADRVYITGNMM--
                                                                                                                                                          FTQTYGGKNSALVF-----NATTP--
                                                                                                                                                                                                  FRSTLTGKNYIMEWYELFQLGNCTFPHLRPEMDAPFWCN----QGAACFFEGIDDVHWK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                               28; Mismatches
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Pred. No. 2.4;
                                                                                                                                                                                                                                                                    Score 94; DB 2; Length 1238; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                               77;
                                                                                                                                                          WANGS I PKSNSTVRFGGYEGVNWG
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                                                                    -NGAQTGGGA--T 588
                                                                                                                                                                                                                                                 96;
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hypothetical protein C06B8.7 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18995
R;Steward, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19057
A;Accession: T18995
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A;Accession: T19604
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                                                                              A;Molecule type: DNA
A;Residues: 1-3036 <WIL>
A;Residues: 1-3036 <WIL>
A;Cross-references: EMBL:Z81463; PIDN:CAB03852.1; GSPDB:GN00023; CESP:C06B8.7
A;Experimental source: clone C06B8
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A;Residues: 1-561 <WIL>
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A;Reference number: Z19150
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A; Map position: 5
A; Introns: 102/3; 157/2;
                                         A; Gene: CESP: C06B8.7
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                                                                                                                                                                                                                                                                                                                                                            T18995
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 LNEVGATEINIA--GATEKNLKTTSQNSYMTFMALGD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                             155 ----YRFYKGDFDLNYDRSQETIHPTLEDLPLQIHDKILKNL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 TWFDSYDCSKFVLRTFNKLAEFGAEFKN--IETNY-----TRIFLYSGEPTYLGNETSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 -WFSVDDANK-----VKKVLDSSSNFKSGIFEVKYCNPLEIAQVF----DPSYAGDTSDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPMKFPFIK----ITYE--
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  288/2; 439/3; 542/1; 591/3; 798/3; 835/3; 1139/1; 1204/3; 1325/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
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-SSGSAKINVSQ 634
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;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
;Accession: F70316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus; Reference number: A70300; MUID:98196666; PMID:9537320; Accession: F70316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ature 392,
                                                                                                                                                                                                                                                                                                                                                                                                                   ;Gene: aq_175
;Superfamily: pro;
;293-486/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Cross-references: GB:AE000677; NID:g2982900; PIDN:AAC06534.1; PID:g2982916; 
;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 1-502 <AQF>
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in: stage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFP-----HLRPEMDAPFWCNQGAACFF
                                                                                            TRIFLYSGEPT-YLG-----
                                                                                                                                                                KWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIETNY 214
                                                                                                                                                                                                                                      GNCTFPHLRPE-MDAPFWCNQGA----ACFFEGIDDVHWKENGTLVQVATISGNMFNQMA
                                                                                                                                                                                                                                                                                                           PIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQL
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                                                        -FLYDGEKTIYLGAKDYARLRELGLVDTLDWGTLKIIVKPLFLFLYWIYEH--TGSWV
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                                                                                                                            -DDLKGINEFEGNIEFGGEESRYFFKGAKDYQKHIVYK----VKLGDKFVSLST--
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                                                                                                                                                                                                    -----HLSVEGLKPPFWVFVGSPPDDEAFYTHVGPV-LKINGEVVRLDV-----
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-QIFDAVIVHKQFYLFYNFEYWFLFMKFPFIKITYEEIPLPIRNKTL 313
                                                                                                                                                                                                                                                                                                                                                                                                                 60% inner membrane protein; III sporulation protein homo
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; Pred. No. 5.4;
51; Mismatches 114; Indels
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; Pred. No. 44;
40; Mismatches 102;
                                                                                            -NETSVFGPTGNKTLGLAIK---RFYYPFKPHLPTKEFL
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                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 502
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                                                                                                                                                                             R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The ColMature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F33E2.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Decies: C-OCt-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T21702
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T21702
                                                                                            A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                      probable aspartic proteinase [imported] - Arabidopsis thaliana (posecies: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change C;Accession: D85056
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                                       A;Gene: AT4g04460
A;Map position: 4
C;Superfamily: or
                                                                                                                                A; Molecule type: DNA
A; Residues: 1-508 < S'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: 284574;
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                                         oryzasin;
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17.9%;
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                                         repeat homology
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1,Pathway: pullulan degradation
1,Pathway: pullulan degradation
1,Note: also has alpha-amylase activity
2,Superfamily: neopullulanase; alpha-amylase core homology
2,Keywords: glycosidase; hydrolase; polysaccharide degradation
1,293-424/Domain: alpha-amylase core homology <AMY>
1,293-424/Active site: Glu, Glu, Asp #status predicted
                                               hypothetical protein Y75B8A.22 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neopullulanase (EC 3.2.1.135) - Thermo
N;Alternate names: alpha-amylase II
T;Species: Thermoactinomyces vulgaris
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A; Residues: 1-585 < TON>
 submitted to the
                    R;Barlow,
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;;Tonozuka, T.; Ohtsuka, M.; Mogi, S.; Sakai, H.; Ohta, T.; Sakano, Y.
;Tonozuka, T.; Ohtsuka, M.; Mogi, S.; Sakai, H.; Ohta, T.; Sakano, Y.
3iosci. Biotechnol. Biochem. 57, 395-401, 1993
A;Title: A neopullulanase-type alpha-amylase gene from Thermoactinomyces vulgaris R-47.
A;Reference number: JC1486; MUID:93222535; PMID:7763540
                                    Accession:
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Matches
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36; Conser
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                                                                                                                                                                                IGMAGAT 464
                                                                                                                                                                                                                                                                                                                                                                 TISGNMFNQMAKWVKQDNETGI----
                                                                                                                                                                                                                                                                                                                                                                                                                                       PHLR---PEMD---
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                                                                                                                                                                                                                    TSVFGPT
                                                                                                                                                                                                                                                      AQGLWNLLDSHDTERFLTSCGGNEAKF
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                                                                                                                                                                                                                                                                                                                             LIVGEIWHDASGWLMGDQFDSVMNYLFRESVIRFFATGEIHAERFDAELTRARMLYPEQA 4C9
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Data Library,
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21.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 6.7;
7; Mismatches
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Pred. No. !
 November
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                                                   15-Oct-1999 #text_change 15-Oct-1999
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A;Accession: T27404
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Redule: type: DNA
A;Residues: 1-1353 <WIL>
A;Residues: 1-1353 <WIL>
A;Cross-references: EMBL:AL033514; NID:e1343251; PIDN:CAA22106.1; CESP:Y75B8A.22
                                                                                                                                                                                                                                                                    A;Title: Cloning and comparative protein modeling of two A;Reference number: Z25292; MUID:20028255; PMID:1056574 A;Recession: T51094 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-465 <DUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: CESP:Y75B8A.22
A;Introns: 28/1; 79/2; 634/3; 996/1; 1134/1; 1296/3
                                    밁
                                                                                                                                                                              A;Gene: pap
C;Superfamily: kidney bean purple acid phosphatase; phosphoesterase
C;Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T51094
R;Durmus, A.; Eicken, C.; Spener, F.; Krebs, B.
Biochim. Biophys. Acta 1434, 202-209, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                 acid phosphatase (EC 3.1.3.2) purple 1, precursor C;Species: Ipomoea batatas (sweet potato) C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000
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Best Local S
Matches 51
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   NVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKNIE--TNYTR--
                                    VYWSENSQHKKVA--KGNIRTYTYFNYTSGYIHHCTIRNLEYNTKYYYEVGIGNTTRSFW
                                                                      VHWKENGTLVQVATISGNM----FNQMAKWVKQ-----DNETGIYYET--
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                                                                                                              Conservative
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                                                                                                                           5.0%; Score 88.5; D
21.4%; Pred. No. 9.7;
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                                                                                                            31;
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Pred. No.
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                                                                                                            ed. No. 9.7;
Mismatches
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         -IFLYSG
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isozymes

Y 172 VKASPEKGAETWFDSYDCSKFVLRTENKLAEFGAEFKNI 21C
Y 116 WCNQGAACFFEGIDDVHWKENGTLVQVATISGNMENQMAKW-VKQDNETGIYYETWN 171
Y 56 QAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFDHLRPEMDAPF 115 :
Y 16 KRFDFRKPDPYCQAKYTFCPTGSPIPVMEGDDDIEVFRL 55 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Query Match 5.0%; Score 88.5; DB 1; Length 1462; Best Local Similarity 20.3%; Pred. No. 42; Matches 71; Conservative 56; Mismatches 115; Indels 107; Gaps 20;
;Gene: GDB:POLA;GDB:120304; OMIM:312040; Cross-references: GDB:120304; OMIM:312040; Map position: Xp22.3-Xp21.1; Superfamily: DNA polymerase; Keywords: DNA binding; DNA replication; nucleotidyltransferase; zinc finger; 654-691/Region: zinc finger CHCC motif; 1249-1374/Region: zinc fingers
;Molecule type: protein ;Residues: 19-37,'C';1406-1425,'C' <hsi> ;Genetics:</hsi>
Res. 18, 6231-623 1 DNA polymerase a 1 imber: S12665; MU 1 1 2 665
idu 88-
;Status: translation not shown; translated from GB/EMBL/DDBJ;Molecule type: DNA
Title: Human DNA polymerase alpha gene: sequences controlling expression in cycling an Reference number: I57513; MUID:91172197; PMID:2005899
; PROTECULE (Type: protectin ; Residues: 438-449;495-502;'G',838-848;1090-1105;1201-1216;1397-1407;1444-1453 <won2> ; Pearson, B.E.; Masheuer, H.P.; Wang, T.S. ol. Cell. Hiol 11 2081-2095 1991</won2>
Human Di ence numbe
sion: S00257; A30440; <u>T</u> 57513; S12665 S.W.; Wahl, A.F.; Yuan, P.M.; Arai, N.; Pearson, B.E.; Arai, K. 7. 37-47. 1988
rected DNA po ies: Homo sap : 30-Jun-1991
ESULT 12
b 253 HVPYKASGSTETEWYSIKRASAYIIVLSSYSAYGKYTPQYKWLEEELDKVNRTETP 308
Y 250 YYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLFWKFPFIKITYEEIP 305
b 193 DLSYADNYPNHDNVRWDTWGRFVERSTAYQPWIWTAGNHEIDFAPEIGETKPFKFFTKRY 25:2
b 145 -FTTPPEVGPD

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A;ILLE: Identification, characterization, and molecular cloning of a novel transporter-1 A;Reference number: S27263; MUID:93050176; PMID:1426240 A;Accession: S27263
                                                                                                                                                                                                   synaptic vesicle protein SV2 - bovine
N;Alternate names: transporter-like protein p87
C;Species: Bos primigenius taurus (cattle)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
A; Molecule type: mRNA
A; Residues: 1-742 < GIN>
                                                                                                    C;Accession: S27263
R;Gingrich, J.A.; Anders
FEBS Lett. 312, 115-122,
A;Title: Identification,
                                                                                                                                                                                                                                                                                                                  S27263
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A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69459
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                                                                                                                                                                                                                                                                                                                                          RESULT 14
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C;Superfamily: hypothetical protein HI0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-411 <KLE>
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
C;Accession: D69459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FF-RIRVYGCRDGE--IFQETRN--ELMEKGTPNFFGLQRFGSIRFITHEVGKLI----- 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EFLLSLLQIFDAVIVHK-QFYLF 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---LQNNYEEAFWVYVAKPFEGENEEVRKIREILWETRDAKLGİRELPKYLRYERNİLQK 235
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Pred. No. 9.2;
45; Mismatches
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A;Cross-references: GB:S47919; NID:g259173; PIDN:AAB24028.1; PID:g259174 C;Superfamily: synaptic vesicle protein SV2

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coxin-like outer membrane protein jhp0556 - Helicobacter pylori (strain J99)
;Species: Helicobacter pylori
;Variety: strain J99
;;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
;;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
;;Accession: D71917
;;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith,
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, Cature 397, 176-180, 1999
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,Residues: 1-3194 <ARN>
,Residues: 1-3194 <ARN>
,Cross-references: GB:AE001488; GB:AE001439; NID:g4155100; PIDN:AAD06134.1; PID:g415510
,Experimental source: strain J99
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.;Accession: D71917
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his SWISS-PROT entry is copyright. It is pretween the Swiss Institute of Bioinformat he European Bioinformatics Institute. The European Bioinformatics Institute. The European Bioinformatics Institutions as long to be and this statement is not removed. Intities requires a license agreement (See or send an email to license@isb-sib.ch). MMBL, AF068227, AAC27614.1; Lenew; HGNC:2076; CLN5.		SEQUENCE FROM N.A., VARIANT VLINCL ASN-279, AND VARIANT ARG-368. TISSUE-Fetal brain; MEDLINE-98324783; PubMed=9662406; Savukoski M., Klockars T., Holmberg V., Santavuori P., Lander E.S., Peltonen L.; "CLM5, a novel gene encoding a putative transmembrane protein mutated in Finnish variant late infantile neuronal ceroid lipofuscinosis."; Nat. Genet. 19:286-288(1998). [2] SUBCELLULAR LOCATION, AND GLYCOSYLATION. MEDLINE-21968572; PubMed=11971870; Isosomppi J., Vesa J., Jalanko A., Peltonen L.; Isosomppi J., Vesa J., Jalanko A., Peltonen L.;	HUMAN CIN5_HUMAN STANDARD; PRT; 407 AA. O7550; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 42, Last sequence update) 10-OCT 2003 (Rel. 42, Last annotation update) Ceroid-lipofuscinosis neuronal protein 5 (CLN5 protein). CLN5. CLN5. CLN5. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. MCBI_TaxID=9606;

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Neopullulanase 2 (I
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Transmem 12
Transmem 308
Transmem 378
Transmem 447
SEQUENCE 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
STRAIN=R-47;
MEDLINE=93222535;
                                 SEQUENCE FROM N.A.,
                                                      NCBI_TaxID=2026;
                                                                                                     Thermoactinomyces vulgaris
Bacteria; Firmicutes; Baci
                                                                                                                                           TVAII
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Q08751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
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                                                                                    Thermoactinomyces.
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InterPro; IPR001708; 60kDa_
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SUBUNIT: Specific
nascent integral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      integration of proteins of the respiratory chain complexes. Involved in integration of membrane proteins that insert dependently and independently of the Sec translocase comple
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                                   AND CHARACTERIZATION
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3.2.1.135) (Alpha-amylase
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34 POTENTIAL.
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Pred. No. 2.2;
$1; Mismatches
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Kamitori S., Abe A., Ohtaki A., Kaji A., Tonozuka T., Sakano Y.;
"Crystal structures and structural comparison of Thermoactinomyces
"ulgaris R-47 alpha-amylase 1 (TVAI) at 1.6 A resolution and
alpha-amylase 2 (TVAII) at 2.3 A resolution.";

J. Mol. Biol. 318:443-453(2002).
-!- FUNCTION: Hydrolyzes pullulan efficiently but only a small amount
of starch. Endobydrolysis of 1.4-alpha-glucosidic linkages in
pullulan to form panose. Cleaves also (1-6)-alpha-glucosidic
linkages to form maltotriose.
-!- CATALITIC ACTIVITY: Hydrolysis of pullulan to panose (6-alpha-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR004185; Glyco_hydro_131g.
InterPro; IPR007110; Ig-like.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02903; alpha-amylase; 1.
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Kamitori S., Kondo S., Okuyama K., Yokota T., Shimura Y., Tonozuka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kamitori
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                                                                                                                                                                                                                                                                                                                                                                                            Carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                    SMART;
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                                                                                                                                                                                                                                                                                                                                                                      3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L; D13178; BAA02473.1; -.

; JC1486; JC1486.

; JC1486; JC1486.

; JC1486; JC1486.

; JC17; 14-MAR-99.

; JUF5; 25-DEC-02.

; JUF5; 25-DEC-02.

; JUT2; 18-DEC-02.

; JUT2; 18-DEC-02.

; JUT2; 18-DEC-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glucosylmaltose).
COFACTOR: Binds 1 calcium ion per subunit.
SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                   MEDLINE=91172197; PubMed=2005899; Pearson B.E., Masheuer H.P., Wang T.S.; "Human DNA polymerase alpha gene: sequences cycling and serum-stimulated cells."; Mol. Cell. Biol. 11:2081-2095(1991).
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Pred. No. 3
                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae
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RUD_ARCFU
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PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA_directed_DNA_polymerase;
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DNA BIND 650 715
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Pfam; PF03104; DNA pol B exo; 1.
PRINTS; PR00106; DNAPOLB.
SMART; SM00486; POLBC; 1.
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Genew; HGNC:9173; POLA.
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- MISCELLANEOUS: In eukaryotes t
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GO:0003889; F:alpha DNA polymerase activity; NAS.
GO:0006260; P:DNA replication; NAS.
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SIMILARITY: Belongs to the DNA polymerase type-B family.
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                                                                                                                                                                                                    FDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYE----EIPLPIRNKTLS
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                       STANDARD;
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation updat.
Probable tRNA pseudouridine synthase D (EC. synthase) (Uracil hydrolyase).
TRUD OR AF1677.
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Pfam; PF01142; UPF0024; 1.
TTTRFAMS; TIGR00094; 1.
TTTRFAMS; TIGR00094; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S. Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B. Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zh. Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR; AF1677; -. ; 1. HAMAP; MF 01082; -; 1. InterPro; IPR001656; UPF0024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tRNA processing; Lyase; Complete proteome.
ACT_SITE 81 81 BY SIMILARITY
SEQUENCE 411 AA; 47715 MW; 109B5250D96
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uracil-13 in transfer RNAs (By similarity).
-!- CATALYTIC ACTIVITY: Uracil + D-ribose 5-phosphate = pseudouridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5'-phosphate + H(2)O.
-!- SIMILARITY: Belongs to the pseudouridine synthase truD family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE=98049343; PubMed=9389475;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota;
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                                                    FKNIETNYTRIF-LYSGEPTYLGNE----TSVFGPTGNKTLGLAIKRFYYPFKPHLPTK
                                                                                                                                                                                                                                                                                                                                                                      SDEGDFLIIRVEKKNW-----DTLNFARVLSNALGISQKRISFAGTKDKRALTVQYFSI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIG-----FRSTLTGKNYTMEWYEL
---LQNNYEEAFWVYVAKPFEGENEEVRKIREILWETRDAKLGLRELPKYLRYERNLLQK
                                                                                                                                                                                 MFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWF--DSYDCSKFVLRTFNKLAEFGAE 206
                                                                                                                                                                                                                                                YGVKK---
                                                                                                                                                                                                                                                                                                              FQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKE---
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                                                                                                                      -IFQETRN--ELMEKGTPNFFGLQRFGSIRFITHEVGKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45;
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Pred. No. 3.8;
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01-OCT-1996
01-OCT-1996
16-OCT-2001
   P7861; Q00744;
15-JUL-1999 (Rel. 38, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chitin synthase D (EC 2.4.1.16) (Chitin-UDP acetyl-glucosaminyl transferase D) (Class-V chitin synthase D).
                                                                                                                                   EMENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matrix protein; Phosphorylation. SEQUENCE 755 AA; 86580 MW; 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSV7J
                                                                                                                CHSD_EMENI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFV-----
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(Rel. 34, Last sequence up)
(Rel. 40, Last annotation)
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                                                                                                                STANDARD;
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MEDLINA--
Motoyama T., Fuja-
Gen. Genet.
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Fungal Genet. Biol. 20:153-167(1996).
-!- FUNCTION: Plays a major role in cell wall biogenesis.
-!- CATALYTIC ACTIVITY: UDP-N-acetyl-D-glucosamine + {(1,4)-(N-acetyl-beta-D-glucosaminyl)}(N) = UDP + {(1,4)-(N-acetyl-beta-D-glucosaminyl)}(N+1).

SUBCELLULAR LOCATION: Plasma membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D83246; BAA11866.2; ~. EMBL; U52362; AAA97482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Motoyama T., Eujiwara M., Kojima N., Horiuchi H., Ohta A., T "The Aspergillus nidulans genes chsA and chsD encode chitin which have redundant functions in conidia formation."; Mol. Gen. Genet. 251:442-450(1996).
                                                                                                                                                                                                                                                                                                                                                Multigene family.
                                                                                                                                                                                                                                                                                                                                                                   Transferase;
                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03142; Chitin synth_2; 1. Pfam; PF00173; heme_1; 1.
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InterPro; IPR001199; Cyt_B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement
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Specht C.A., Liu Y., Robbins P.W., Bulawa C.E., Ia:
Winter K.R., Riggle P.J., Rhodes J.C., Dodge C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FGSC
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                                                                                                                                           Similarity 20.5
75; Conservative
                                                             TYC---SVITFWAPDFVLKCFGMPQKAQRSAWREKIG-LISIILMIAAFVGFLTFGFTAT
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BELONGS TO THE CHITIN SYNTHASE :
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iwara M., Kojima N.,
253:520-528(1997).
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496
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wara M., Kojima N.,
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                                                                                                                                                                4.9%;
                                                                                                                                                                                                                         133504 MW;
-GKNYTMEWYELFOLGNCTFPHLR--PEM----DAPF-WCNQGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kojima N., Horiuchi
ne EMBL/GenBank/DDBJ
                                                                                                                                             44;
                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
D06157184F154EDE5 CRC64;
                                                                                                                                                              Score 87; DB
Pred. No. 18;
                                                                                                                                             Mismatches
                                                                                                   -RLQAPVWEFKYGDLLGHLKIMHDAIGFRS---TLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                   В
                                                                                                                                                                                   1;
                                                                                                                                             132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H., Ohta A
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eurotiomycetes,
                                                                                                                                                                                 Length 1184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY. SUBFAMILY CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iartchouk N.,
L., Culp D.W.,
                                                                                                                                                                                                                                                                                                                                                                       Cell
                                                                                                                                               Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohta A.,
                                                                                                                                                                                                                                                                                                                                                                       wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takagi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takagi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthases
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              commercial
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                           123
                                                                                                         85
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28-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, I
15-MAR-2004 (Rel. 43, I
3-0x0-5-alpha-steroid 4
5-alpha-reductase 2) (S
                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type II
Nucleic
                                   GO; GO:0003865; F:3-oxo-5-alpha-steroid 4-dehydrogenase GO; GO:0030539; P:male genital morphogenesis; IMP. GO:0006694; P:steroid biosynthesis; IMP. InterPro; IPR001104; Strd5A_dhC. Pfam; PF02544; Steroid dh; I. Pfam; PF02544; Steroid dh; I. PROSTIE; PS50244; SSA_REDUCTASE; 1. Oxidoreductase; Microsome; Transmembrane; Sexual differe
                                                                                                                              9,99,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differentiation and androgen physiology (By similarity).
-!- CATALYTIC ACTIVITY: A 3-oxo-5-alpha-steroid + acceptor =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q99N99;
                                                                                                                                                                                                                   EMBL; AB049456; BAB40179.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Transcriptional regulation of the mouse steroid 5alpha-reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takeyama K., Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21882004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRD5A2 OR 5ART2
                                                                                                                                                                                                                                                                                                                                                                                                                                          intracellular membrane (By similarity). SIMILARITY: Belongs to the steroid 5-alpha reductase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       delta(4)-steroid + reduced acceptor.
SUBCELLULAR LOCATION: Integral membrane protein. Microsomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eic Acids Res. 30:1387-1393(2002).
FUNCTION: Converts testosterone into 5-alpha-dihydrotestosterone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and progesterone or corticosterone into their corresponding alpha-3-oxosteroids. It plays a central role in sexual
                                                                                                                                                                                                MGI:2150380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene by progesterone in brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNQQI 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FYYPEKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEEIPLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NVKASPEKGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFEGID------DVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETW 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACHTSGSARKSFYSLKNSGDVYFTWEDTKNTSR-----KLAVYSGNVLDLNLLNWFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQVNYPTKFKDLRDNDDIRGVDLTYYFQTGEDKQIGKCLSQIIKVGSIDTDTVGCIASQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FFQEVNGACKGLITRTENSDIPTNSNGDLAWY--FPCHAFNQDGS--SEPNTTVSYYNGW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCGTPPTRLKINEIGSGYMIFHGQAYDLTKSTHPAAAGIPDMTNVLYDLPHKYGGQDGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                Srd5a2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=11884637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Last sequence update)
, Last annotation update)
d 4-dehydrogenase 2 (EC 1.3.99)
(SR type 2) (5 alpha-SR2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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                                       Transmembrane; Sexual differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LYSGEPTYLG---NETSVFGPTGNKTLG-LAIKR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; l
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -TWEDSYDCSKEVLRTENKLAEFGAE----FKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5) (Steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a 3-oxo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus.
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BPH1_YEAST
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         RA Carignani G., Chanet R., Contreras R., Crouzet M., Daignan-Fornier B., Rh De Haan M., Defoor E., Delgado M.D., Demolder J., Doira C., Dubois E., Rh Dujon B., Duesterhoeft A., Esrdmann D., Esteban M., Fabre F., Bairhead C.A., Faye G., Feldmann H., Fiers W., Rh Fairhead C.A., Faye G., Feldmann H., Fiers W., Rh Francingues-Gaillard M.-C., Franco I., Frontali L., Fukuhara H., Rh Goffeau A., Grenson M., Grisanti P., Gilliquet V., Glansdorff N., Rh Fuller L.J., Gent M.E., Gigot D., Gilliquet V., Glansdorff N., Rh Hatat D., Hegemann J.H., Herbert C.J., Hilger F., Hohmann S., Rh Hollenberg C.P., Huse K., Iborra F., Indge K.J., Isono K., Jackman P., Augg C., Jacquet M., James C.M., Jauniaux J.-C., Jia Y., Jimenez A., Augg C., Jacquet M., James C.M., Jauniaux J.-C., van der Linden C.G., Rh Lucchini G., Lutzenkirchen K., Maat C., Mannhaupt G., Manzano M.E., Rh Airtegani E., Mathieu A., Maurer C., T.C., McConnell D., McKee R.A., Rh Messenguy F., Mewes H.-W., Molemans F., Montague M.A., Navas L., Rh Messenguy F., Mewes H.-W., Molemans F., Montague M.A., Navas L., Rh Messenguy F., Mewes H.-W., Molemans F., Montague M.A., Navas L., Rh Poetsch B., Pohl F.M., Purnelle B., Ramezani Rad M., Rasmussen S.W., Ra Raynal A., Renacha M., Richterich P., Roberts A.B., Rodriguez F., Rh Shu Y., Sala J., Slonimski P.P., Sor F., Soustelle C., Thierry A., Shala J., Stateva L.I., Steensma H.Y., Steiner S., Thierry A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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TRANSMEM
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Sanz E., Schaall-Gerbrunger, Sor E
Shu Y., Skala J., Slonimski P.P., Sor E
sniegelberg R., Stateva L.I., Steensma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92244356; PubMed=1574125;
Oliver S.G., van der Aart O.J.M., Agostoni-Carbone M.L., Aigle M.,
Alberghina L., Alexandraki D., Antoine G., Anwar R., Ballesta J.P.
Benit P., Berben G., Bergantino E., Biteau N., Bolle P.-A.,
Belle P.-A.,
Bolotin-Fukuhara M., Brown A.J.P., Brown R., Buhler J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P25356; Q02396; Q07348;
01-MAY-1992 (Rel. 22, Created)
10-QCT-2003 (Rel. 42, Last sequence update)
10-QCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rodriguez F., Martegani E., Mauri I., Alberghina "The sequence of 8.8 kb of yeast chromosome III c PM3270 contains an unusual long ORF (YCR601).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beige protein homolog 1.
BPHI OR YCR032W OR YCR591 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92116648; PubMed=1837415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales; Saccharomycetaceae; NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BPH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=S288c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yeast 7:631-641(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNKLAEFGAEFKNIETNY----TRIFLYSGE-PTYL-----GNETSVFGPTGNKTLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FGKPASYGKHSESVSSGVPLLPARIAWFLQELPSFVVSVGMLAWQPRSLFGPPGNVLLGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FSAHYFHRTFIYSLLTRGRPLSAVIFLKATAFCIGNGLLQAYYLVYCAEYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
92
166
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the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wicksteed B.L., Roberts A.B., Sagliocco F.A., Brown A.J.P., "The complete sequence of a 7.5 kb region of chromosome III Saccharomyces cerevisiae that lies between CRY1 and MAT.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91335897; PubMed=1872032;
Jia Y., Slonimski P.P., Herbert C.J.;
"The complete sequence of the unit YC
                                                                                                                                                                     DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X59075; CAA41798.1; -. EMBL; S78624; AAB21258.1; -. PIR; S19444; S19444. Germonline; 138938; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zimmermann F.K., Sgouros J.G.;
"The complete DNA sequence of yeast chromosome III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thireos G., Triano L.N., Urrestarazu I.A., Valle G., Vetter I., van Vliet-Reedijk J.C., Volckaert G., Vreken P., Warmington J.R., von Wettstein D., Wicksteed B.L., Wilson C., Wurst H., Xu G., Zimmermann F.K., Sgouros J.G.;
                                                                                                                                                                                                                                      Repeat;
                                                                                                                                                                                                                                                                              PROSITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X62452; CAA44309.1; -.
EMBL; X59720; CAC42982.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: May be involved in acetic acid export.
-!- SIMILARITY: Contains 1 BEACH domain.
-!- SIMILARITY: Contains 4 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast 7:761-772(1991)
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                                                                                                                                                                                                                                                                                                      ProDom; PD007848; Beige_BEACH; PROSITE; PS50197; BEACH; 1.
                                                                                                                                                                                                                                                                                                                                 Pfam; PF02138; Beach; 1.
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InterPro; IPR000409; Beige_
InterPro; IPR001680; WD40
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PS50294; WD_REPEATS_REGION; 1.
PS50082; WD_REPEATS_2; FALSE_NEG.
                                                                           FWCNQGAACFFEGIDDVHWKENG-TLVQVATISGNMF---NQMAKWVKQDNE-----
DNTSLDFKIKKSISRYTYNLKTDREENAVFYRNNLNLLIFHLKHTLEIQSNPNSSCKWSS
                       --TGIYYE-----TWNVKASPEKGAETWFDSYDCSKFVLR-----TFNKLAEFGA
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Pred. No. 7
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  (See http://www.isb-sib.ch/announce/
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029067;
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                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                            reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VC-16
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=2234;
                                                                                                                                                                                             Hypothetical protein; Complete proteome. SEQUENCE 228 AA; 27209 MW; 3B29C4F593A26B68 CRC64;
                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                TIGR; AF1201; -.
                                                                                                                                                                                                                                                             EMBL; AE001021; AAB90048.1;
                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of the hyperthermophilic,
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                             227 -LGNETSVFGPTGNKTLGLAIKRFYXPFKPHLPTKEFLL--SLLQIFDAVIVHKQFYL 281
                                                                                             169 TWNVKASPEKGAETWFDSYDCSKFVLR-TFNKLAEFGAEFKNIETNYTRIFLYSGEPTY-
                                                                                                                               29;
                                                                                                                                                Similarity
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                                                                 -FHPTTSCVDYYLRIEFKKLFELCKIMKNMKTKMVRLGTYVSQDAYK
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Pred. No.
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28-FEB-2003 (Rel. 41, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of 13 novel transcripts and the human RGS8 gene from the 1q25 region encompassing the hereditary prostate cancer (HPC1) locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sood R., Bonner T.I., Makalowska I., Stephan D.A., Robbins C.M., Connors T.D., Morgenbesser S.D., Su K., Faruque M.U., Pinkett H., Graham C., Baxevanis A.D., Klinger K.W., Landes G.M., Trent J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
PURELIVE alpha-mannosidase Clorf22 (EC 3.2.1.-).
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01532; Glyco_hydro_47; 1.
Pfam; PF02225; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:16787; Clorf22.
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                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000886; ER_target_S.
InterPro; IPR001382; Glyco_hydro_47.
InterPro; IPR003137; PA.
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                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Hydrolase; Glycosidase; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00747; GLYHDRLASE47.
                                                                                                                                                                                                                                                                                                        Endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. SIMIIARITY: Belongs to family 47 of glycosyl hydrolases.
140 AKQLGYKLLPAFNTTSGLPYPRINLKFGIRKPEARTGTETDTCTAC
                            100
                                                                                   44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF288393; AAG60613.1;
                                                                                                                65;
                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF 16-469 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73:211-222 (2001).
                                                                                   MEGDDDIEVERLQAPVWEFKYGDLLG--HLKIMHDAIGFRSTLTGKNYTMEWY--ELFQL
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75
152
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468
468
767
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                                                                                                                  Conservative
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20.6%;
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                                                                                                                                                                        MW;
                                                                                                                41;
                                                        -LGGLLGGHSLAIM
                                                                                                                               Score
Pred.
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                                                                                                                                                                                                                    N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                   Mismatches 108;
                            -NCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG
                                                                                                                                                                          21354A62C5901666
                                                                                                                                 Nо.
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27;
                                                                                                                                           Length 889;
                                                                                                                                                                           CRC64;
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HGPB_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                    <del>: :</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ACTS AS A RECEPTOR FOR HEMOGLOBIN OR THE HEMOGLOBIN/HAPTOGLOBIN COMPLEX OF THE HUMAN HOST AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gam Pasteurellaceae; Haemophilus. NCBI_TaxID=727;
                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Conservation of hemoglobin/hemoglobin-haptoglobin binding Haemophilus influenzae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Ela / Serotype B;
Morton D.J., Stull T.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren Z., Jin H., Morton D.J., Stuil T.L.;
"hgpB, a gene encoding a second Haemophilus influenzae hemoglobin-hemoglobin-binding protein.";
Infect. Immun. 66:4733-4741(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hemoglobin and hemoglobin-haptoglobin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGPB
                                                   EMBL; AF022910; AAC60790.1; -. EMBL; AF259266; AAK51630.1; -.
                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=H1689 / Serotype B;
MEDLINE=98427137; PubMed=9746572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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               InterPro; IPR006970; PT.
InterPro; IPR000531; TonB_boxC
                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Outer membrane.

RISCELLANEOUS: THIS PROTEIN IS SUBJECT TO PHASE-VARIABLE EXPRESSION ASSOCIATED WITH ALTERATION IN THE LENGTH OF THE CCAR REPEAT REGION. THIS MECHANISM IS CALLED SLIPPED-STRAND MISPAIRING. ADDITION OR LOSS OF CCAA REPEAT UNITS WOULD CHANGE THE READING FRAME AND RESULT IN INTRODUCTION OF STOP CODONS DOWNSTREAM OF THE FRAME AND RESULT INSTRODUCTION OF STOP CODONS DOWNSTREAM OF THE REPEAT REGION. THIS MAY BE A MECHANISM OF REGULATION AND A REPEAT REGION. THE INMINIOLOGICAL RESPONSE OF THE HOST.

SIMILARITY: BELONGS TO THE TONB-DEPENDENT RECEPTOR PROTEIN FAMILY; HEMOGLOBIN/HAPTOGLOBIN BINDING PROTEIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR HEME UPTAKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAFTTDFRVHWAQHPL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKFPF-IKITYEEIPL 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLAIKRFYYPFKPHLPTKEFLLSLLQIF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVHI-----HKPMLNARTWMDALLAFFPGLQVLKGDIRPAIETHEMLYQVIK-KHNFLP
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Matches 71
FDXG_HAEIN
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PROSITE; PS00430; TONB_DEPENDENT_REC_1; FALSE_NEG.

PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.

Outer membrane; Transport; TonB box; Multigene family; Signal;
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                            304
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                                                                                                                                                                                                                                                                                                                  16 KRFDFRPKPDPYCQAKYTFC----PTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGH
                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                         RGITPKLPDDIVKGLFIPLP
                                                                                                             ANLCPRVDPEFSYLLPI----KTTGKSVYLFDNLVITDYLSFDLGYRYDNIHYQPKYK
                                                                                                                                                                  GAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFY-----YPFK 254
                                                                                                                                                                                                                                           WCNQGAACFFEGI----DDVHWKENGTLVQVATISGNMFNQMAK------
                                                                                                                                                                                                                                                              SNGETYDFKKFIDTDKKVIED-----KLTLKNPNDTWYDC-SIFNCE---
                                                                                                                               PHL----
                                                                                                                                                                                     ERLWQERDLDTNTQQLNLDLTKDFKTWHIEHNLQYGG----SYNTA--MKRMVNR----
                                                                                                                                                                                                                         --NNAKIKVFEGNYSYGYDGKWKE--VDLEIKTLNGKKFAKIKDPTNKIKSILPSSPGYL
                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created) (Rel. 32, Last seq
                                                                                                                                                                                                      WVKQDNETGIY-----YETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEF
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                             AA;
                            STANDARD;
                                                                                                                                                                                                                                                                             -PTKEFLLSLLQIFDAVIVHKQFYLFYNF---EYWFLPMKFPFIKITYEE---
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Last sequence update)
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I -> V (IN STRAIN EIA).

D -> N (IN STRAIN EIA).

T -> K (IN STRAIN EIA).

T -> K (IN STRAIN EIA).

T -> K (IN STRAIN EIA).

T -> S (IN STRAIN EIA).

G -> A (IN STRAIN EIA).

G -> A (IN STRAIN EIA).

N -> D (IN STRAIN EIA).

N -> P (IN STRAIN EIA).

R -> H (IN STRAIN EIA).

R -> H (IN STRAIN EIA).

R -> G (IN STRAIN EIA).

R -> G (IN STRAIN EIA).

S -> G (IN STRAIN EIA).
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Pred. No.
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                                                                         677
                                                                                          307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                 -AGNDASDVQWWATPTLGY---NFYDQPYTCATAYSWN
                                                                                                                                                                                                                                                                                                                                      Mismatches 105;
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C-TERMINAL
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                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOX.
                                                                                                                                                                                                                                                                                                                                                       Length 999;
                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutron G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Fhillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                         Pfam; PF04879; Molybdop_Re4S4; 1.
Pfam; PF00384; molybdopErin; 1.
Pfam; PF01568; Molydop_binding; 1.
TIGRPAMS; TIGR01553; formate-DH-alph; 1.
TIGRPAMS; TIGR01409; TAT_signal_seq; 1.
PROSITE; PS00551; MOLYBDOPTERIN PROK 1; 1.
PROSITE; PS00490; MOLYBDOPTERIN_PROK 2; PALSE_NEG.
PROSITE; PS00932; MOLYBDOPTERIN_PROK 3; 1.
Oxidoreductase; Molybdenum; Selenocysteine; Selenium; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDIJINE=9535630; PubMed=7542800;
MEDIJINE=9535630; PubMed=7542800;
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                                                                               Oxidoreductase; Molybdenum; Se
Iron-sulfur; 4Fe-4S; Complete
METAL 50 50 51
METAL 53 53 I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              active-site selenocysteine is encoded by the opal codon, UGA. May bind a 4Fe-4S cluster.

SUBUNIT: FORMATE DEHYDROGENASE IS A MEMBRANE-BOUND COMPLEX, FORMED BY SUBUNITS ALPHA, BETA AND GAMMA.

SUBCELLULAR LOCATION: Cytoplasmic (Potential).

SUBCELLULAR LOCATION OF BOTH E.COLI FDNG AND FDOG.

SIMILARITY: Belongs to the prokaryotic molybdopterin-containing
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009010; Asp_decarb_fold.
InterPro; IPR006443; Formate-dh-alph.
InterPro; IPR006657; Mol_dinuc_bind.
InterPro; IPR006963; Molybdop_Fe484.
InterPro; IPR006655; Prok_Mboxred.
InterPro; IPR006655; Prok_Mboxred.
InterPro; IPR006311; Tat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U32686; -; NOT_ANNOTATED_CDS
TIGR; HI0006; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- COFACTOR:
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Pasteurellaceae; Haemophilus.
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COFACTOR: Molybdenum (molybdopterin) and selenocysteine.

COFACTOR: Molybdenum is encoded by the opal codon,
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                                                                             Lee N., Brewer H.B. u..,
"Human liver apolipoprotein B-100
derived amino acid sequence.";
""" Natl. Acad. Sci. U.S.A. 83:f
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Knott T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, East sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) [C
B-48 (Apo B-48)].
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Gotto A.M. Jr.,
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MEDLINE=88003974; P
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                                                                                                                                                                                 MEDLINE=87041416; Pub
Law S.W., Grant S.M.,
  MEDLINE=87161758;
Cladaras C., Hadzo
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87008488;
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                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E.H., Blackhart B.D., Pierotti V.R., Caiati L., T., Scott J., Mahley R.W., Levy-Wilson B., McCar equence of the human apolipoprotein B gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                               Chem.
                                                                                                                                                                                                                                                                                                                                                 Yang C.-Y., Chen Jr., Chan L.;
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  1758; PubMed=3030729;
Hadzopoulou-Cladaras
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                                                                                                                                                                                                                                                                                                                           CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Res.
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                                                                                                                                                                                                                                                                               261:12918-12921(1986)
                                                                                                                                                                                                                                                                                                                                                                                               PubMed=3759943;
                                                                                                                                                                                 PubMed=3464946;
M., Higuchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=3652907;
                                                                                                                                                                                                                                                                                                                           and amino acid sequence
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Primates;
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Catarrhini; Hominidae;
                                                                                              83:8142-8146(1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         n B., McCarthy gene.";
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  R.T.,
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    Atkinson
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MEDIINE=88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W.,
Silberman S.R., Cai S.-J., Deslypere J.P., I
Gotto A.M. Jr., Li W.-H., Chan L.;
"Apolipoprotein B-48 is the product of a mes
specific in-frame stop codon.";
Science 238:363-366 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-291 FROM N.A.
SEQUENCE OF 1-291 FROM N.A.
MEDLINE-86149325; PubMed-3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J.,
Protter A.A., Hardman D.A., Schilling J.W., Miller J.,
Protter A.A., Hardman D.A., Schilling J.W., Miller J.,
Protter A.A., Hardman D.A., Schilling J.W., Miller J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lu "Human apolipoprotein B: identification of cDNA clones and characterization of mRNA.";
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                                                                                                                                                                                                                                                        PARTIAL SEQUENCE, MEDLINE=88018019;
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Knott T.C., Pease R.J., Powell L.
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Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.; "Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100."; Nature 323:738-742(1986).
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Cunny G., Cambien F., Roizes G.;
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AND ILE-3921.
MEDLINE=98141125; PubMed=9490296;
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Arveiler D., Marques-Vidal P., Luc G., Roizes G., C
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-!- FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons, VLDL and LDL. It functions as a recognition signal for the cellular binding and internalization of LDL particles by
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                                Q8a3v2 bacteroides
Q8nbj6 homo sapien
Q8iau5 plasmodium
Q8ia4 plasmodium
Q9zv89 arabidopsis
Q13785 homo sapien
Q9tym2 caenorhabdi
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Q8c157 dictyosteli
Q8cjg6 dictyosteli
Q8nihl trichophyto
 Q8whw9 psilotum nu
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to ceroid-lipofuscinosis, neuronal 5 (Fragment).
                                                                                                                                                                                                                                                                              EMBL; BC025487; AAH25487.1;
MGD; MGI:2442253; Cln5.
                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia;
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                                                                                                   LLGHLKIMHDAIGFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFE 126
                                                                                                                                                       SRRHWPVPYKRFDFRKPDPYCQAKYTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGD
                                                GIDDVHWKENGTLVQVATISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDS
                                                                                 LLGHFKLMHDAVGFRSTLTGKNYTIEWYELFQLGNCTFPHLRPDKSAPFWCNQGAACFFE
YDCSKFVLRTFNKLABFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAI 246
                           GIDDKHWKENGTLSVVATISGNTFNKVAEWVKQDNETGIYYETWTVRAGPGQGAQTWFES
                                                                                                                                       SGQRWPVPYKRFSFRPKTDPYCQAKYTFCPTGSPIPVMKDNDVIEVLRLQAPIWEFKYGD
                                                                                                                                                                                                                                                      336 AA; 38911 MW;
                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                            80.9%; Score 1423; DB 11; 79.4%; Pred. No. 3.1e-116;
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Q86I57;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Similar to CEROID-LIFOPUSCINOSIS neuronal protein 5
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Nature 420:563-573(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Olfactory brain; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                 KKFYGDERPYLSTKDELMNFLKIEDTVIIHRQFYLFYNFEYWFLFMKDPFVKITYEETPL
                                                                                                                                                      KRFYYPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLFYNFEYWFLPMKFPFIKITYEBIPL
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  (TrEMBLrel.
                          PRELIMINARY;
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Pred. No. 8e-116;
"" cmatches 35;
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Best Local S
Matches 54
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  Matches
                                            EMBL; AC116982; AAO51609.1;
Hypothetical protein.
SEQUENCE 378 AA; 42306 M
                                                                                                                                            MEDLINE=22092622; PubMed=12097910;
Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                         Q86JG6
Q86JG6;
                                                                                Submitted (MAR-2003) to the
                                                                                             Baumgart C
                                                                                                           STRAIN=AX4;
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                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyosteliida;
NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                                           Hypothetical protein
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01-JUN-2003
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EMBL, AC116305; AA052280.1; -.
Hypothetical protein.
SEQUENCE 180 AA; 20631 MW; 2DEB686F4FBC11A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A. "Sequence and analysis of chromosome 2 of Dictyostelium discoideum." Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Dictyostelium discoideum (Slime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baumgart C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=AX4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyosteliida;
                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22092622; PubMed=12097910;
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 l Similarity
65; Conserv
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                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUNDPELCQQRIQREDCPQ-TPVPWGTFNDNDEIEVYYMQAPVFEAVFGNFFGKLGGYHS
                                                                                                                                                                                                                                                                                                                                                                                                                   KNIYSTASKTYMGTÍNGTQLNQYIEWMQQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                        EN----GTLVQVATISGNMFNQMAKWVKQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIGFYDLTTGLNYTAEYDAFFEVGNGTLPNIINVDGKDELLWCNAGILCTVPYINETYWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIGFRSTLTGKNYTMEWYELFQLGNCTFPHL--RPEMDAPFWCNQGAACFFEGIDDVHWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKPDP-YCQAKY--TFCPTGSPIP--VMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHD
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  Conservative
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                                              42306 MW;
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          11.5%;
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                                                                       ŀ
Score 202; DB
Pred. No. 2.4e-
53; Mismatches
                                                                                 EMBL/GenBank/DDBJ
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Last
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Pred. No. 1.2e-12;
5; Mismatches 60
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        DB 5;
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                       Length 378;
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Best Local S
Matches 61
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GO; GO:000422; F:metalloendopeptidase activity;
GO; GO:0008270; F:zinc ion binding; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; I
InterPro; IPR001842; Peptidase_M36.
InterPro; IPR006025; Pept M_Zn_BS.
Pfam; PF001228; Peptidase_M36; I.
Pfam; PF001228; Peptidase_M36; I.
PRINTS; PR00999; FUNGALYSIN.
PROSITS; PR00999; FUNGALYSIN.
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metalloprotease; SEQUENCE 633 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Capoccia S., Lechenne B., Zaugg C., Monod M., "Trichophyton rubrum encoding metalloprotease Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
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                      NKLAEFGAEFKNIETNYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIKRFYYPFKPHL
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                                                                                                                                                                                                                                                                                                                 QAPVWEFKYGDLLGHLKIMHDAI-----GFRSTLTGKNYTMEWYELFOLGNCTFPHL
                                                                       NVVDYVSHATYQVYRWPIPDPTEGKREIVENPWNLKTSP----FTWISDGKTNYTTTRGN
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                                                                                                                                                                                                                                                                   -EKRDFSGPMRAFHGACKALNLPINADKATI---
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A; 69778 MW;
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22.8%;
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Last annotation updat
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Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                     KEDGTLALTWRVETDMGDNWLLSYVDAKETDKVH
                                                                                                                       IYYETWNVKASPEKGAETWFDSYDCSKFVLRTF
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 633;
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Best Local S
Matches 52
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STRAIN-VPI-5482 / ATCC 29148;

STRAIN-VPI-5482 / PATCC 29148;

MEDLINE-22550858; PubMed=12663928;

Xu J., Bjursell M.K., Himrod J., Deng S., Car.

Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides thet
Science 299:2074-2076 (2003).

EMBL; AR016937; AA077958.1; -
GO; GO:0004553; F:hydrolase activity, hydroly
GO; GO:0005975; P:carbohydrate metabolism; IE
 SEQUENCE FROM N.A. Ota T., Nishikawa T., Saito K., Yamamoto J.,
                                                                                                       01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003
01-JUN-2003
01-OCT-2003
                                              NCBI_TaxID=9606
                                                           Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                 Hypothetical protein NT2RP2002760.
Homo sapiens (Human).
                                                                                                                                 Q8NBJ6;
01-OCT-2002
                                                                                                                                                          9ranað
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR006710; Glyco_hydro_43.
Pfam; PF04616; Glyco_hydro_43; 1.
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                                                                                                                                                                                                                                                                                                                                                                                   WPVPYKRFDFRPKPDPYCQAKYTFCPTGSPIPVM--EGDDDIEVFRLQAPVWEFKYGD--
                                                                                                                                                                                                                                       QMAKWVKQDNETGIYYETWNVKASP-EKGAETWFDSYDCSKFVLRTFNKLAEFGAEFKN
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                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                         PRELIMINARY;
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                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          58155 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      5.7%;
 Suzuki Y.,
Wakamatsu
                                                                                                                                                                                                                                                                                                                                     -LLGHLKIMH-----DAIGFRSTLTGKNYTMEWYE-----LFQL
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                                                                                                          Last sequence update)
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Last annotation update)
                                                                                                                                  Created)
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Pred. No. 3
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Kawai-Hio
A., Nagai
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Э.
Т.
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                                                                                                          update)
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 Hayashi K.,
Nakamura Y.
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             Ishii
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Matches 57
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GO; QQ
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"HRI human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00083; sugar_tr; 1.
TIGRENMS; TIGRO1299; synapt_SV2; 1.
PROSITE; PS50859; NFS; 1.
PROSITE; PS00217; SUGAR_TRANSPORT_2;
PROSITE; PS00217; SUGAR_TRANSPORT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR005828; Sub_transporter.
InterPro; IPR005829; Sug_transporter.
InterPro; IPR005988; SV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QBIAU5;
01-MAR-2003
01-MAR-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Transmembrane.
SEQUENCE 682 AA; 76660 MW; D1A76C115424CC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007114; MFS
                                                                                                                                                                                                                                                                                                                                                                                              PF08_0094.
Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8IAU5
                                                                                             PROSITE;
                                                                                                                                                                                EMBL; AL844507; CAD51265.1; --
GO; GO:0007049; P:cell cycle;
InterPro; IPR001373; Cullin.
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Seeger K., Murphy L., Harris D., Berriman M.,
Quail M., Barrell B.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cullin-like
                                                                                                                     Pfam; PF00888; Cullin; 1.
SMART; SM00182; CULLIN; 1.
PROSITE; PS50069; CULLIN_2; 1.
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                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTLVQVATISG-NMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFV
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, putative.
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       Conservative
                                                                                               AA;
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           51;
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           Score 97.5; DI Pred. No. 9; 51; Mismatches
                                                                                                                                                                                                                       IEA
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                115;
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                                                                                                         CRC64;
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                                                           Length 804;
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                   Indels
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                     65;
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01-MAR-2003
01-MAR-2003
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Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Harris B., Lennard N., Clark L., Line A., Barron A., Corton C., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Dogge Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; ALM44509; CAD52545.1; -.

Hypothetical protein.

Hypothetical protein.

SEQUENCE 508 AA; 58842 MW; F563E34ClA9F25D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Alveolata;
NCBI_TaxID=36329;
[1]
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PF13_0225.
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Q9ZV89;
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Pred. No. 6.7;
33; Mismatches
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(TrEMBLrel.

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Matches
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01-JUN-2003 (
APOB protein
WEDLINE=86042646; PubMed=2932736; Wei C.F., Chen S.H., Yang C.Y., Marcel Sparrow J.T., Gotto A.M. Jr., Chan L.; "Molecular cloning and expression of p
                                                                                                                                                                                APOB
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                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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Q13785;
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Vysotskaia V.S., Schwartz J.R., Toriumi M., Yu G., Li J.,
Kremenetskaia I., Luros J., Araujo R., Buehler E., Conwar
Dewar K., Feng J., Kim C., Li Y., Shinn P., Davis R.W.,
Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC F9X20 sequence.";
"Arabidopsis thaliana chromosome 1 BAC F9X20 sequence.";
                                                                      SEQUENCE
                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                   01-NOV-1996
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosiceurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                           TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                 284
                                                                                                                                                                                                                                                                                                                                                                                                                251
                                                                                                                                                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                 YPGRPN
                                                                                                                                                                                                                                                                                                                                                                                                               YPFKPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFKIALTIWSKWIDHNIDPSKTRVFYQGVSPVHLNGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLILKLDSISRGNQWLGSDVAIFNTFHWW----SHTGRAKTW-DYFQTGDKIVKEMNRME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFF---EGIDDVHWKENGTLVQVAT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTFCPTGSPIPVMEGDDDIEVFRLQAPVWEFKYGDLLGHLKIMHDAIGFRSTLTGKNYTM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YRWQPTGCDIPRFNGRDFLTRFKGKKILF---VGDSLSN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                              (TrEMBLrel. 01, 01) (TrEMBLrel. 01, 1) (TrEMBLrel. 24, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Columbia;
                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                                                                                                                                                                                                                                                                                                                256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SCMLHAAVPNAKYTFQLNKGLSTFTIPEYGI-SVNFLKNGFLVDLVSDKTR 171
                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40568 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KNIETNYTRIFLYSGEPTYL-GNETSVFGPTGNKTLG--LAIKRFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10,
24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last
Last
                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 95.5;
Pred. No. 4
                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A9887DD29786278B CRC64;
                                   Marcel Y.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence update)
 partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                   Milne R.W., Li W.H.,
   CDNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G., Li J., Liu
E., Conway A.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                WGKPGKTCLGETVPVQGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
   and
   deduced amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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XX MEDLINE-Berkeley;

XX MEDLINE-20196006, pubMed=10731132;

XX MEDLINE-20196006, pubMed=10731132;

XX MEDLINE-20196006, pubMed=10731132;

XX Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

XX Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

XX Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

XX Adams M.D., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

XX George R.A., Lewis S.E., Richards S., Ashburner M., Pfeiffer B.D.,

XX George R.A., Lewis S.E., Yandell M.D., Zhang Q., Chen L.X.,

XX Ash M.D., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

XX Aman K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

XX Aman K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

XX Aman K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

XX Aman K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

XX Aman K.H., Doyle C., Baxter E.G., Helt G., Nelson D.,

XX Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

XX Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

XX Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

XX Borkova D., Botchan M.R., Bouck J., Bayraktaroglu L., Beasley E.M.,

XX Borkova D., Botchan M.R., Bouck J., Bavensport L.B., Davies P.,

XX Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

XX Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dlunkov B.C., Dunn P.,

XX Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

XX Aman M., Glasser K.,

XX Aman M., Glasser K.,

XX Aman M., Glasser K.,

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XX Aman M., Glasser M.,

XX A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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EMBL; M12413; A
PIR; A27850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
CG3696 protein (KISMET-L long isoform).
KIS OR CG3660 OR CG3696 OR CG18326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9VPL9; Q9NI64;
01-MAY-2000 (Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEZ
GO; GO:0005215; F:transporter activity;
GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VPL9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000531; TonB_boxC.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
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B-100.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFPGKPGIYTREELCTMF-IREVGTVLSQVYSKVHNGSEILFSYFQDLVITLPFELRK 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYPEKPHLETKEFLLSLLQIEDAVIVHKQFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EWKDKAQNLYQELLTQEGQASFQGLKDNVFDGLVRVTQEFHMKVKHLIDSLIDFLNFPRF 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFKNIETN-YTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAIK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TQIKVNWEEEAASGLLT--SIKDNVP-----KATGVLYDYVNKYHWEHTGLTLREVSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVHWKENG-TLVQVATI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGSPIPV-----MEGDDDIEVFRLQAPVWEFKYGDLLG---HLKIMHDAIGFRSTLTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRRNLQDHAEWVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDCSKFVLRTFNKLAEFGA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSAPSPAVGTVGMDMDEDDDFS-----KWNFYYSPQSSPDKKLTIFKTELRVRESDEE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      836 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acad. Sci. U.S.A. 3; AAA51742.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96317 MW; 5298C27EE21AB140 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GAIREIDDIDERFQKGASGTTGTYQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82:7265-7269(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -LFYNFEYWFLPMKFPFIK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                              W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -RF 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415
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A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
JALIU M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
A Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
A Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
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                   EMBL; ABO03590; AAF51257.3; --
EMBL; AF215703; AAF51267.3; --
HSSP; F231570; IAPO
FlyBase; FBgn0001309; kis.
GO; GO:0000785; C:chromatin; IEA.
GO; GO:0005524; F:ATP binding; I
GO; GO:0008026; F:ATP dependent
GO; GO:0008026; F:ATP dependent
GO; GO:0003682; F:Chromatin bind
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                                                                                                                                                                                                                                                                                                                                                                                        "A Genetic Screen for Modifiers in Drosophila.";
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Adams M.D., Cein.
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SEQUENCE FROM N.
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GO:0000785; C:chromatin; IEA.
GO:0005634; C:nucleus; IEA.
GO:0005524; F:ATP binding; IEA.
GO:000526; F:ATP dependent helicase activity; IEA.
GO:0003682; F:chromatin binding; IEA.
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4AR-2000) to the EMBL/GenBank/DDBJ
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of a K
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RESULT 13
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ID Q9TYM2
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DT 01-MA
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Pfam; PF00271; helicase C; 1.
Pfam; PF00176; SNF2 N; T.
SMART; SM00298; CHROMO; 2.
SMART; SM00490; HELICC; 1.
SMART; SM00490; HELICC; 1.
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Wat. Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Wat. Matson A. Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9TYM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Y25C1A.7 OR Y25C1A
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ATP-binding; Helicase; Hydrolase.
SEQUENCE 5322 AA; 573615 MW;
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GO:0006333; P:chromatin assembly/disassembly; IEA.
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Last
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update) annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
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Query Match
Best Local S
Matches 48
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01-JAN-1998
01-JAN-1998
01-JUN-2003
       pylori.";
Nature 388:539-547(1997).
Nature 388:539-547(1997).
                                                                                              Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G., Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams N.D., Hickey E.K., McKenney K., FitzGerald L.M., Lee N., Adams N.D., Hickey E.K., Betg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=26695 / ATCC 700392;
MEDLINE=97394467; PubMed=9252185;
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                            Helicobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 025330
                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori (Campylobacter
                                                                  "The complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF125459; AAD12838.1; PIR; T33904; T33904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted [3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans.";
Nature 368:32-38(1994).
[2]
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Pfam; PF04893; Yip1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WormPep; Y25ClA.7a; CE21474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
A64596; A64596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FC-NLSHGFLTNGNLKTGSFSEQKMNFYTSFITSASTLIFL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLGNETSVFGPTGNKTLGLAIKR---FYYPFKPHLPTKEFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPFWVSV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMHDAIGFRSTLTGKNYTMEWYELF-----QLGNCTFPHLR-----PEMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 05, (TrEMBLrel. 05, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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C. elegans cosmid Y25ClA.";
99) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                              Helicobacter
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21.7%;
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Epsilonproteobacteria;
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Pred. No.
                                                                     οf
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                                                                    the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1238
                                                                  gastric pathogen
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on update)
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                                                                                                                                                                                                                                                                                                                                                         Campylobacterales;
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                                                                    Helicobacter
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                                                                       Query Match
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Best Local
                                                                                                                                                 InterPro; 1rave-1.
Pfam; PF00004; AAA; 1.
Pfam; PF05095; DUF825; 1.
PROSITE; PS00589; PTS HPR SER; 1.
PROSITE; PS00589; PTS HPR SER; 1.
Profical protein; Chloroplast.
273575 MW; E
                                                                                                                                                                                                                                                             Psilotum nudum.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AP004638; BAB84296.1; --
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005521; F:sugar porter activity; IEA.
GO; GO:000531; F:sugar porter activity; IEA.
GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar ph
InterPro; IPR003959; AAA ATPase_centr.
InterPro; IPR008543; DUF825.

InterPro; IPR008543; DUF825.
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01-MAR-2002
01-MAR-2002
01-OCT-2003
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Wakasugi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moniliformopses;
NCBI_TaxID=3240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Moniliformopses; Psilotophyta; Psilotales; Psilotaceae; Psilotum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Psilotum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. YCF2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vakasugi T., Nishikawa A., Yamada K., 'Complete nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    589
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                        79
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                                                                                           Similarity
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GFRSTLTGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCNQGAACFFEGIDDVH----WK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nudum (Whisk fern).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FKFQGKTTIEKSVLSDASYTFDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDFYDWTGGGYDFTGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRFY-----YPFKPHLPTKEFLLSLLQIFDAVIVHKQFYLF-----YNFEYW-FLPMK 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNFVGATEINIA--GATFKNLKTTSQNSYMTFMALGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKFYLRTFNKLAEFGAEFKNIET---NYTRIFLYSGEPTYLGNETSVFGPTGNKTLGLAI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTGYITGTFTADRVYITGNMM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTLYQVAT----ISGNMFNQMAKWVKQDNETGIYYETWNVKASPEKGAETWFDSYDC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRSTLIGKNYTMEWYELFQLGNCTFPHLRPEMDAPFWCN----QGAACFFEGIDDVHWK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FTQTYGGKNSALVF----NATTP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kingyoku;
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                        5.3%;
21.7%;
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                                                                  ; Score 94; DB; Pred. No. 72; 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GVFDSVNFNKAYYKFQGTENSYNFKNTNFLAGN
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                                                                                                                                                             FE005DF98460C03E CRC64;
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chloroplast
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                                                                  103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --WANGSIPKSNSTVRFGGYEGVNWG 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77;
                                                                                                            Length 2313
                                                                                                                                                                                                                                                                                                                                                   sugar phospho.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1238;
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